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(54) Title: SHORT CHAIN DEHYDROGENASES/REDUCTASES (SDR)

(57) Abstract: The present invention relates to a method for identifying or verifying members of the short chain dehydrogenase (SDR) family, to a method for providing modulators for members of the SDR family and to the preparation of pharmaceutical agents using these modulators.

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Short chain dehydrogenases/reductases (SDR)

Description

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The present invention relates to a method for identifying or verifying members of the short chain dehydrogenase (SDR) family, to identified SDRs, to a method for providing modulators for members of the SDR family and to the preparation of pharmaceutical agents using these modulators.

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Technical Background

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The short chain dehydrogenase/reductase (SDR) protein family (H. Jörnvall et al., Biochemistry 34 (1995), 6003-6013) is an old conserved protein family, the members of which show a residue identity level of only 20-30%. However, it has been found that the three-dimensional structure of members of the SDR family are highly similar, determining their functions and affiliation to the SDR family (U. Oppermann et al., Enzymology and Molecular Biology of Carbonyl Metabolism 6, Weiner et al. eds., Plenum Press, New York (1996), p. 403-415).

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While initially only two structures of SDR enzymes restricted to bacterial and insect enzymes have been discovered, rapid progress on the knowledge of short chain dehydrogenases/reductases resulted in an increasing number of structures, which could be assigned to the SDR family. Currently, about 1.600 putative members are known, from which up to 100 may be derived from human, such as hydroxysteroid dehydrogenases (HSD).

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An approach to identify SDR proteins is described in W.N. Grundy et al., Biochemical and Biophysical Research Communications 231 (1997) 760-766 and in T.L. Bailey et al., J. Steroid Biochem. Molec. Biol. 62 (1) (1997)

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29-44. Therein homologies are searched for via a hidden Markov model, i.e. a self-training model, and thus classified to a certain protein family. A classification based on the function is not made in these models.

5 Since the SDR enzymes are involved in various metabolic pathways and show different activities, such as oxidoreductases, lyases, or epimerases and, as discussed above, show only a low identity of 20-30%, it has been difficult, to assign new members unambiguously to the SDR family and to find modulators therefor.

10

However, since HSD and other SDR play a critical role in higher vertebrates, it is desirable to discover further members of the SDR family and establish modulators for known and new SDR enzymes.

15 It was therefore an object of the present invention to provide an algorithm which allows for the identification or verification of SDR family members with high confidence levels.

20 It was a further object of the invention to provide an algorithm which provides a search hierarchy with various levels.

It was another object of the present invention to provide modulators for SDR family members.

25 Still another object of the invention was to provide pharmaceutical agents based on members of the SDR family.

Summary of the invention

30 The present invention relates to a method for identifying or verifying members of the short chain dehydrogenase (SDR) family based on an algorithm using core SDR motifs for searching members of the SDR family.

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Further, the present invention relates to a method for providing modulators for such members of the short chain dehydrogenase (SDR) family, which enhance or inhibit the activity therefrom as well as a method for providing a pharmaceutical agent using modulators for members of the SDR family.

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In particular the present invention provides a combination of the steps (i) screening databases to search and find SDR sequences, (ii) store the data on an appropriate medium, rank and validate the hits and (iii) using the SDR sequences found to develop new drugs.

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Detailed description of the invention

Members of the SDR protein family have a common core sequence, which is about 250-350, preferably about 260-290 and in particular about 270 amino acids in length. SDR proteins can have extensions at the N-terminus and/or at the C-terminus. Typically, these extensions have a length of 20 to several hundred, in particular up to 500 amino acids. These extensions can be membrane anchors or other signals or they can constitute completely distinct protein domains. Therefore, according to the invention it is primarily searched for SDR core domains, the rest of the protein being analysed only later on.

In a first embodiment the invention provides a method for identifying or verifying members of the short chain dehydrogenase (SDR) family comprising the steps

- (a) providing a target sequence of molecules to be classified,
- (b) comparing said target sequence with core SDR motifs selected from
 - (i) MV1 being derived from the motif MT1:TGxxxGxG by replacement of 0 to 2 amino acids,
 - (ii) MT2:NN(0-2:x)AG,
 - (iii) MT3:N, located at a position 90-110 relative to MT1,

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- (iv) MV4 being derived from the motif
MT4:S(11-52:x)YxxxK by replacement of 0-2 amino acids and
 - (v) MT5:PG,
- 5 (c) determining positive SDR candidates containing
 - (i) at least the core SDR motifs MV1 and MV4 and
 - (ii) at least 7 of the 14 amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5 and
- 10 (d) classifying positive SDR candidates as belonging to the SDR family.

It has been found in many SDR proteins that several motifs of the SDR core domain often occur in combination. However, it is not obligatory that all SDR core motifs are present for a protein to be an SDR enzyme. Since 15 SDR proteins may lack one or several of the core SDR motifs, they may not be found by simple comparison of the complete SDR core domains.

Within the SDR core the following functional motifs frequently are found. The motifs are given in order from N-terminus to C-terminus assigning a 20 position number 0 to the start of the first motif MT1, which of course need not be the start of the complete SDR protein.

MT1:TGxxxGxG (circa position 0-7);
MT2:NNAG (circa position 75-78);
25 MT3:N (circa position 100);
MT4:S-Y-K (circa positions 128/142/146) and
MT5:PG (circa position 170/171).

Using these motifs, the algorithm according to the invention has been 30 developed, which allows for an assignment of target sequences to be an SDR sequence with a confidence level of more than 95%, in particular more than 98%. By relying on motifs of the core SDR region positive hits

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due to identity in non significant regions can be excluded. It is essential for the present invention that the core SDR motifs were selected because of their functional meaning and not only because of homology comparisions. The SDR motifs used form essential parts of nucleotide co-factor binding region (Rossman-fold) and the active site of members of the SDR family. The motifs MT1 and MT2 represent components of the co-factor binding site. A particular co-factor of SDR enzymes is NAD(P)(H). The motif MT3 represents a contact to the active site and the motif MT4 a part of the active site. The motif MT5 is of functional importance due to its proximity to the co-factor. Thus core SDR motifs are motifs which are essential for the functionality of the SDRs.

For detecting members of the short chain dehydrogenase (SDR) family in the method according to the invention it is therefore essential that functional aspects are considered, wherein enzymatically active SDRs are detected and not only sequences which exhibit a certain homology to other SDRs at functionally irrelevant positions.

Contrary to prior art algorithms, according to the invention those amino acids are taken into account which are essential for the function. A minimum amount of the amino acids selected thus enables a maximum amount of targets due to the divergence of the SDR family, wherein the detection of erroneously positive targets is basically excluded because of the connection between function and structure. This way the target specificity can be considerably improved over algorithms, such as neuronal networks, which are based on homology comparisons (cf. J.A Gerlt et al., Genome Biology, 1 (5) (2000), Reviews 0005.1-0005.10). In addition, further functional information can be easily included in order to screen for functional deficits, such as screening for an associated disease mutations or individualized drug metabolism.

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While the individual proteins assigned to the SDR family using the algorithm of the invention may have identities of only 30% or less, they show a very similar three-dimensional structure. It is important for the correct formation of the desired three-dimensional SDR structure that
5 motifs 1 to 5 are present in the above listed succession.

For the description of the motifs the single letter amino acid code is used.
x denotes a variable amino acid, selected preferably from the 20 naturally
occurring amino acids. NN(0-2:x)AG means that 0, 1 or 2 amino acids can
10 be positioned between amino acids N and A. S(11-52:x)YxxxK means that
from 11 to 52 amino acids are positioned between S and Y and 3 amino
acids are positioned between Y and K.

A replacement of 0-2 amino acids refers to a replacement of any of the
15 amino acids given (including x), whereby preferably the explicitly named
amino acids are replaced. A replacement includes deletion of the amino
acid or a substitution of the amino acid by another amino acid selected
preferably from the 20 naturally occurring amino acids. The replacement of
1 or 2 amino acids results in a fuzzy logic including also sequences, in
20 which the motifs are not 100% conserved. A strategy combining sequence
and structure information is also disclosed by L. Yu et al., Protein Science
7 (1998), 2499-2510.

In a preferred embodiment of the invention MT2 is defined to be NNAG
25 (i.e. without any amino acids x between NN and AG), but with possible
replacement of 1-3 amino acids.

The motif MT3:N is located at position 90-110, preferably at position 95-
105 and in particular at position 100 relative to the start of the motif MT1.
30

In a particularly preferred embodiment of the invention the second part of
motif MT4 is defined to be the pattern YxASK with possible replacement of

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up to 3 of these residues. In this preferred embodiment the range of possible scores is extended from 0-14 up to 0-16. In this embodiment positive candidates have a score of at least 7, preferably at least 9, more preferably at least 11 and most preferably at least 13.

5

Preferably the SDR motifs are located in the order given from the N-terminus to the C-terminus for a sequence to be classified as SDR sequence. The positions given in brackets above may be shifted by amino acid insertions or deletions within the sequence analyzed. Preferably the motifs are found within \pm 50, more preferably \pm 20 positions, in particular \pm 10 positions and most preferably \pm 5 positions, from the values given.

10

A target sequence is classified as belonging to the SDR family according to the invention, if it contains at least the core SDR motifs MV1 and MV4 and at least 7 of the 14 explicitly named amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5. The confidence level can be controlled by varying the amount of matching amino acids, which have to be present in the target sequence. Therefore, if a high confidence level, e.g. > 98%, more preferably > 99% is desired, it may be preferable to classify target sequences as positive SDR candidates, only if they contain at least 9 of the 14 amino acids, or even at least 11 or at least 12 of the 14 amino acids contained in the motifs MT1-MT5. Setting the score at a value of at least 13 results in the detection of exclusively sequences, which are an SDR with a confidence level of almost 100%, e.g. >99.8%.

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In a preferred implementation of the method of the invention a file is provided containing a set of protein amino acid sequences, the input set. One sequence is taken from the input set, the query sequence. The implementation then passes the query sequence to the algorithm, which examines it for occurrences of some or all of MT1-5 in the arrangements allowed. The algorithm returns a list of the best possible combinations of

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occurrences. If the matches contain more than a specified number of amino acids from MT1-5, they are assigned as hits.

5 In a particularly preferred embodiment the method of the invention is as follows:

10 The algorithm first searches the whole sequence for instances of the first motif MT1, allowing for up to two replacements as described. Each possible MT1 match is then taken as the origin for searches for the motifs
10 MT2 to MT5 whose positions are defined relative to the position of MT1. A data structure based on each position of MT1 is created, which will be used to store the positions of other motifs relative to this MT1.

15 For a given MT1 match at position P, the preferred position of the motif MT2 is P + 75. According to the rules MT2 is preferably at position (P + 75) +/- 50, more preferably (P + 75) +/- 20. This defines a window on the sequence within which instances of the motif MT2 are searched for, including any variants of MT2 with up to three replacements. Since the size of the window affects the time taken to search and the quality of the
20 matches found, the preferred implementation allows the window sizes to be specified for each search. Any possible matches within the window are added to the result data structure as children of the current MT1.

25 The procedure is then repeated for instances of MT3, where the window is (P + 100) +/- 50, more preferably (P + 100) +/- 20, or any other specified window size. Again, any results found within the allowed window are added to the result data structure as children of the current MT1.

30 The same procedure is then followed for MT4, with a window (P + 128) +/- 50, more preferably (P + 128) +/- 20, or any other specified window size. In this case the window only specifies the position of the Serine residue of MT4, and once a candidate Serine has been found at position P_s (and

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added to the result structure as a child of the current MT1), it defines a window $P_s + (11-52)$, within which instances of the second part of MT4 are searched for, allowing for replacements. Any candidates are added to the result structure as children of the current Serine match.

5

Since MT4 allows replacements, and those replacements could include replacements of the Serine, the implementation additionally searches for the second part for MT4 in cases where the Serine is not found. In this case, a virtual window composed of all of the possible positions of the (missing)

- 10 Serine, offset by the $P_s + (11-52)$, is constructed $[P_s + (11-52) +/- 20$, i.e. the range $P + 128 + (11-20)$ to $P + 128 + (52+20)]$, or likewise for any specified window size. If any instances of the second part are found they are added to the result data structure as children of the current MT1.
- 15 The procedure is then repeated for instances of MT5, where the window is $(P + 170) +/- 50$, more preferably $(P + 170) +/- 20$, or any other specified window size. Again, any results found within the allowed window are added to the result data structure as children of the current MT1.
- 20 At this stage the implementation holds in memory a tree-structured data structure where the possible matches with the specified pattern correspond to depth-first traversals of the tree. The implementation enumerates the possible combinations of the full or partial motifs, adds up a score calculated from the number of residues in the motifs which were actually matched, and discards the instances where the overlapping windows have given rise to motifs where the ordering is not MT1-MT2-MT3-MT4-MT5.
- 25 Any combination with a score equal to the maximum score found is kept and added to a list, and it is this list with its score, the motifs found, and the position in the sequence of each amino acid matched which is returned
- 30 as the result at this stage of the implementation.

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The preferred implementation includes significant enhancements, in particular:

- MT2 is defined to be NNAG without the presence of 1 or 2 amino acid insertions between the NN and AG parts. The implementation allows for replacement of 1-3 of the residues, and will continue to search for other motifs even if no instance of MT2 is found.
- The second part of MT4 is defined to be the pattern Y*ASK instead of Y**K, but again the implementation allows replacement of up to 3 of these residues. This makes the range of possible scores 0-16 instead of 0-14.
- The absence of motif MT4 is not used to discard SDR candidates, but the effect on the overall score of its absence (5 out of a possible 16 matches) is significant in excluding matches which do not contain it and additionally the presence of the active site MT4 tyrosine is indicated for each result, as a significant indicator of possible SDR catalytic activity.

In a further preferred embodiment an enlargement or optimization, of the algorithm is performed also on human extended SDRs. Thus it is taken into account that compared to the other SDRs often only a motif MT_x1 ($TGxxGxxG$) as well as a motif MT_x4 ($YxxxK$) is present, wherein MT_x1 is a variant of $TGxxxGxG$. For determining human extended SDRs with this enlarged algorithm motifs 2, 3 and 5 can even be missing.

- 25 In a particularly preferred embodiment the algorithm according to the invention comprises the import of a data set, e.g. from data bases, organizing the data set by using the method according to the invention, ranking the SDR hits and further analyzing and managing the data of the detected hits, such as a cross-linking to data bases, to BLAST or to other tools.

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Subject matter of the invention is also a data carrier, particularly a diskette containing the method according to the invention and particularly the above described algorithm.

5 Whereas the method according to the invention itself already has a very high specificity and reliability in the selection of SDR candidates, the SDR candidates detected can be subjected to further evaluation criteria. These criteria are e.g. comparing the 3D-structure of the candidates detected with the 3D-structure of known SDR proteins or a standardized 3D-
10 structure, which is derived from SDR candidates identified by the method according to the invention. Thus, in a further preferred embodiment of the invention the polypeptides classified as positive SDR candidates in the method according to the invention are subjected to another evaluation step in view of their three-dimensional structure in order to further improve the
15 selectivity and specificity of the method. Thus it is possible to use known three-dimensional structures of SDR family members (cf. e.g. H. Jörnvall, Biochemistry 34 (1995), 6003-6013; U. Oppermann et al., Adv. Exp. Meth. Biol. 414 (1997), 403-415 or J. Benach et al., J. Mol. Biol. 282 (1998), 383-399). However, it is also possible to determine the three-
20 dimensional structures of the SDR candidates detected with the method according to the invention and to prepare a common comparative three-dimensional structure therefrom. This way it can be examined, e.g. whether the positive SDR candidates exhibit the co-factor binding site typical of SDRs. A further criteria may be the presence of amino acid Y at
25 position 152 ± 20 , particularly ± 10 . Further, it is possible to compare the amino acids sequences detected with known SDR sequences, e.g. via an alignment.

After the sequences have been classified as SDRs it is also possible to
30 search for further domains, e.g. membrane domains in order to thus classify them to a certain type of tissue.

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An important subgroup of SDRs are FabGs, which are derived from pathogens and which can be identified via the method according to the invention. Since FabGs are often strongly degenerated and thus exhibit a relatively low score (e.g. 9 or more) in the method according to the invention, it can be advantageous to examine possible FabG-SDR candidates in a second step in view of the presence of the following motif variations: MT_y2:VxVNAG, wherein V can be replaced particularly by I, as well as MT_y5:PGFI, wherein F and/or I can be missing.

- 10 A list of FabG proteins which were identified by the method according to the invention is shown in Table 4. FabGs are involved in the lipid metabolism of bacteria and are particularly suitable for the development of antibiotics.
- 15 A further group of SDRs which can be identified by the method according to the invention are bacterial SDRs. Bacterial SDRs detected with the algorithm according to the invention are shown in Table 3.

20 Further, it is possible to detect production enzymes as well as thermostable enzymes with the method according to the invention.

25 In a most preferred embodiment, the so-called SDR_Finder, the method according to the invention is based on the implementation of functional data both on the three-dimensional structure and on the biological function (NADP(H)-dependend enzymes). The implementation is hierarchically structured according to the smallest common denominator having a functional meaning. Contrary to known tools not motifs, but SDR candidates are searched for and thus also for those having a very low homology or hardly conserved core motifs, respectively. The search for 30 SDR candidates according to the invention enables a considerably higher specificity. The SDR candidates detected are of biologically functional

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relevance. At the same time a greater number of hits is found due to the use of the smallest common denominator.

Further, it is possible to establish a ranking with the algorithm according to
5 the invention, to export the data in different formats and to selectively search for species. Thus, the SDR_Finder represents an "all-in-one" analysis solution including various obtainable possibilites, particularly the worldwide web. The implementation of hyperlinks to NCBI, EMBL and their tools (e.g. Blast, ClustalW, Pfam, PDB, Medline, OMIM) represents an "in
10 silico" analysis/drug development software of modular structure which is particularly developed for SDR. Further modules which can be connected thereto are the examination of three-dimensional structures, the determination of active centres and the substrate docking simulation. The latter can also be implemented directly into the SDR_Finder and allow
15 direct access, e.g. to 3D-databases and chemical libraries via the worldwide web.

In a preferred embodiment the SDR_Finder is equipped with fuzzy logic.

20 In addition, experimental data can be used, e.g. to evaluate the exchange of one amino acid in a motif regarding the functional consequences. This is of importance both for the individual adjustment of therapies and the evaluation of pathological problems or for the development of diagnostica, respectively.

25 Moreover, it is possible to enlarge the algorithm subgroup-specifically, as is shown herein for the FabG_SDRs.

30 The method according to the invention can be used to verify sequences, which are already classified as (putative) SDR sequences, e.g. by automatic alignment (BLAST), to belong to the SDR family or not. Further, it can be used to search for and find new members of the SDR family or to

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search for and find new isoforms of SDR proteins. Therefore, the method of the invention provides additional information with regard to known sequences as well as to novel sequences. From the knowledge that a target sequence belongs to the SDR family as well as from the information 5 obtained from the ranking findings about substrates and functions can be obtained. An important selection criteria thereby is the drugability of the SDR candidates detected.

The method according according to the invention can be used to detect 10 e.g. human SDRs (human extended SDRs), animal SDRs, particularly mammalian SDRs, but also bacterial SDRs, FabG_SDRs, fungi SDRs, SDRs of pathogens, SDRs of parasites, e.g. plant parasites.

The SDR proteins classified with the algorithm according to the invention 15 thus can serve as platform for novel drug development. Human SDR proteins can particularly serve as starting point for the treatment of diseases or malfunctions of the body, whereas bacterial SDRs particularly provide a starting point for the development of novel antibiotics. Further, respective SDRs can serve for the development of antimicotic, 20 pesticides, herbicides etc...

While the algorithm of the present invention preferably is used to search 25 for protein sequences, it is also possible the convert the motifs given into nucleic acid sequences and screen nucleic acid databases. A method to convert amino acid sequences into nucleic acid sequences while considering the degeneration of the genetic code is e.g. given from H. Jörnvall, FEBS Letters 456 (1999), 85-88. A search on the nucleic acid level can preferably be used to preselect sequences, which are then confirmed by an alignment in the protein level.

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For the search on nucleic acid level these protein sequences are preferably converted to DNA sequences in particular cDNA sequences and used for

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the detection of further SDR candidates via a fuzzy logic or a hidden Markov model or via neuronal networks.

5 The method of the invention therefore also provides a tool for preselection of SDR candidates on the genomic level.

Preferably a ranking of the positive SDR candidate is performed e.g. according to the number of amino acids matching with motifs MT1-MT5. This way a hierarchy and/or an evolutionary relationship of the obtained 10 SDR candidates can be obtained.

In a particularly preferred embodiment the target sequences classified as positive SDR candidates contain at least the core SDR motifs MT1 and MT4.

15 By hierarchically classifying the verification of the individual core SDR motifs several levels to detect SDR proteins can be obtained.

By using the algorithm according to the invention the search for SDR 20 candidates and consequently the development of pharmaceuticals can be decisively enhanced. So far for the production of pharmaceuticals in vitro tissue cultures were admixed with different substrates. From cultures, wherein a certain substrate was converted, the target protein was isolated. According to the invention, this step and thus the knowledge of a 25 substrate for the development of inhibitors or for the development of pharmaceuticals is not necessary. Moreover, starting from the sequence found a modulator, in particular an inhibitor or activator can be derived. This modulator can e.g. be derived from known modulators of other, in particular of related SDR proteins, suitable substrates, related functions 30 and tissue distribution for 17 β HSD isoforms are described e.g. by H. Peltoketo et al., J. Molecular Endocrinology 23 (1999), 1-11. Further, it is possible to derive a modulator from the 3D-structure of the SDR sequence.

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Such a 3D-structure can be obtained experimentally, e.g. by X-ray chrystallography or by computer based calculations, e.g. ab initio, force field, or rule based methods. Further, by inhibiting the active site of the SDR protein the function thereof can be determined.

5

The searching for SDR family members and ranking is also applicable to evaluate lead-candidates for possible inhibitors or modifiers of a specific enzyme. Leads may be derived from metabolites of evolutionary closely related or very distant enzymes from other species, if the same metabolite 10 may not be found in the respective target organism. The evolutionary relationship of SDRs and their distinction from MDRs (medium chain dehydrogenase) is e.g. described by H. Jörnvall et al., FEBS Letters 445 (1999), 261-264 and AKRs (T.M. Penning, Endocrine Rev. 18(3) (1997) 281-305).

15

SDR enzymes are often involved in intermediary metabolism, as well as in hormone and mediator metabolism.

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Substrates of known SDR proteins include e.g. steroids, such as estrone/estradiol, cortisone/cortisol and testosterone/3 α -androstenediol. Thus, after classifying a sequence as SDR sequence functional tests for steroid substrates result in higher hit rates.

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Further substrates of SDR proteins are UDP-glucose, UDP-N-acetylglucosamine, sepiapterin, dihydropteridine, R-3-OH-butyrate, dienoyl CoA, trans-Enoyl CoA, fatty acids, L-3-OH-acyl CoA. These substrates are particularly converted of SDR enzymes, which are involved in the intermediary metabolism. Further substrates of SDR proteins, particularly of SDR enyzmes, which are involved in hormone, mediator and xenobiotic 30 metabolisms, are several hydroxy steroids, e.g. 3-beta-hydroxysteroids, 11-beta-hydroxy steroids or 17-beta-hydroxy steroids as well as prostaglandines and retinoides.

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Further, searching SDRs, ranking and comparing evolutionary patterns can also be used to detect clinically relevant polymorphisms and/or single nucleotide polymorphisms (SNPs). This approach can be used to characterize disease mechanisms as well as metabolism of xenobiotics,
5 e.g. drug metabolism.

The identification of SDR members, ranking and comparing evolutionary patterns also allows for the identification of structure-function relationships. These structure-function relationships are a key for
10 identification of substrates of ORFs with unknown functions.

Within a lead oriented characterization first binding of a positive SDR candidate is evaluated. Starting from the binding a modulator, e.g. an inhibitor or activator, can be developed. Useful information for developing
15 an inhibitor can be obtained from protein sequence alignment of full-length sequences, e.g. by comparison with known SDRs. Further, valuable information can be obtained from expressed sequence tags (EST) and gene sequence comparison. The procedure using the algorithm according to the invention allows for a great reduction of possible modulator candidates to
20 be analysed and practically excludes target sequences, which are not SDR sequences. Therefore, an analysis of the functions in vitro or in vivo can be performed with much less effort than in the state of the art due to the reduced number of compounds to be tested. While in the methods according of the state of the art often the substrate must be known, this
25 knowledge is not essential for developing modulators or/and drugs according to the invention. It is even possible to derive possible substrates in a subsequent step from the functions of the SDR enzymes found according to the invention. Ligands can be derived according to the procedure described by G.R. Lenz et al., DDT, 5(4) (2000), 145-156.

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The validation of the potential SDRs found according to the algorithm of the invention, which can be used as new targets for drug development,

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can then be performed by experimental biochemical methods, such as high-throughput function screening for function identification, ultra high-throughput screening for lead compounds, transfection assays, knock out experiments, microarrays, tissue expression, cDNA arrays or analysis of
5 disease in animal or in vitro model systems. However, it is also possible to use virtual methods using e.g. computers for validation of the new targets, e.g. by molecular homology modelling or substrate docking simulations.

Suitable strategies include e.g. gene expression of an identified SDR
10 protein to obtain the protein molecule and subsequently performing biological functional assays and observe the behaviour of the cell.

Alternatively, the 3D-structure may be derived from the SDR sequence and
15 an inhibitor for the active site provided. Using the inhibitor the function of the SDR within an organism can be evaluated.

Small weight inhibitors for SDR enzymes, which can be used as starting point for developing new or modified inhibitors, in particular inhibitors for newly identified SDR enzymes include:

20 1) Steroidal-based inhibitors like steroid carboxylates, acrylates, enolates 3,4-and 16,17-fused ring pyrazoles, 3 alpha, 17-beta or 20-beta-spiro-oxiranes as well as steroidal spirolactones, progestins, ursodexycholate, synthetic analogs of estrone sulfate and estrone-3-amino derivatives.

25 2) Inhibitors based on flavonoides and dihydropterin derivatives.

30 3) Inhibitors based on polyphenols and derivatives of 2,3-dihydroxy-1-naphthoic acids like gossypol (1,1',6,6',7,7'-hexahydroxy-5-5'-diisopropyl-3,3'-dimethyl-2,2'-binaphthalene-8,8'-dicarbaldehyde).

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4) Inhibitors based on glycyrrhizin (3beta,20beta)-29-hydroxy-11,29-dioxoolean-12-en-3-yl 2-O-beta-D glucopyranuronosyl-alpha-D-glucopyranosiduronic acid) and components of enzymatically hydrolysed licorice extract like 3-O-beta-D-glucoronopyranosyl-24-hydroxy-18beta-glycyrrhetic acid, 3-O-beta-D-glucur-onopyranosyl-18beta-glycyrrhetic acid and 3-O-beta-D-glucuronopyranosyl-18beta-liquiritic acid, monoglycosylated derivatives of glycyrrhizin as well as carbenoxolone.

5) Pharmaceutically acceptable salts of the above mentioned molecules

such as alkali metal (e.g. sodium), alkaline earth metal (e.g. magnesium) or ammonium as well as salts of organic carboxylic acids, such as acetic, citric, oxalic, lactic, tartaric, malic, isothionic, lactobionic, ascorbic and succinic acids; organic sulfonic acids, such as methanesulfonic, ethanesulfonic, benzenesulfonic and p-tolysulfonic acids; and inorganic acids, such as hydrochloric, sulfuric, phosphoric, and sulfamic acids.

Further candidates for inhibitors are chalcones (cf. Life Sci 68 (7) (2001) 751-761) as well as phytoestrogens (cf. Life Sci 66 (14) (2000) 1281-1291) and frenolicin and its derivatives.

20 Further, inhibitors can be derived from 3D-structures of the SDRs found, confirmed, identified or verified with the method of this invention, as is described e.g. by Liao et al., Structure, Vol. 9 (2001) 19-27.

25 Since SDR enzymes, in particular human SDR enzymes have been found to be involved in many pathways of the body, they are outstanding targets for developing new drugs. In particular human SDR enzymes have been found to be involved in intermediary metabolism, lipid mediator/hormone metabolism or xenobiotic phase I metabolism. On the other hand, SDR enzymes often constitute pathogenic factors causing diseases. Thus, e.g. the AME syndrome is associated with 11 β HSD-2, bile acid metabolism is associated with 3 β HSD, polycystic kidney disease is associated with

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Ke6(17 β HSD-8) and Alzheimer's disease is associated with ERAB(17- β HSD-10).

Further diseases which can be effected by influencing, modulating or

5 inhibiting SDRs comprise e.g. DHPR deficiency, phenylketonuria, dienoyl CoA reductase deficiency, galactosemia III, tetrahydrobiopterine deficiency, adrenal hyperplasia, adrenogenital syndrome, 11-oxoreductase deficiency, apparent mineralocorticoid excess syndrome, ovarian/breast cancer, male pseudohermaphroditism, Zellweger syndrome, pregnancy/ovarian cancer, 10 polycystic kidney disease, Alzheimer's disease, retinitis punctata albescens, retinitis pigmentosa, Down's syndrome, arterial hypertension, oncogenes, follicular lymphoma, hepatocarcinogenesis, aging related hormone deficiencies and immunity in general.

15 Since many of the SDR enzyme are bidirectional (reversible oxidoreaction) depending on the environment, it is also possible to provide a means for selectively enhance one of the enzymatic reaction, i.e. oxidation or reduction or to reverse the action observed.

20 Thus, providing new SDR sequences and modulators therefor, as described above, allows for the preparation of drugs or pharmaceutical agents, which can be used to control many different diseases. In particular drugs for treatment of cancer, e.g. breast cancer or prostate cancer, obesity, diabetes, fertility, osteoporosis, glucose metabolism, or conditions related 25 to aging can be prepared. Further applications include steroid resistance, in particular estrogen resistance and glucocorticoid resistance.

30 Further, SDR proteins and in particular hydroxy steroid dehydrogenases (HSDs) are outstanding targets for tissue-specific modulation of hormone-dependent or sensitive diseases, e.g. cancer, in particular prostate or breast cancer.

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The present invention is in particular useful for providing a pharmaceutical agent for affecting immune regulation is provided by developing a modulator for 17 β HSD type 3, 17 β HSD type 7, 17 β HSD type 8, 17 β HSD type 10, 11 β HSD-1, CR1, UDP glucose epimerase, SDR_SRL,
5 AF067174, AF151840, AF151844, AF0078850, Fvt-1, HEP-27, DKFZ_ORF, WWOX_ORF, or CR3, a pharmaceutical agent for affecting autoimmunity is provided by developing a modulator for 17 β HSD-3, 17 β HSD-8, 11 β HSD-1, AF057034, U89717, CR1, AF0078850, HEP-27, or
10 CR-3, a pharmaceutical agent for wound healing or partial recovery is provided by developing a modulator for 17 β HSD-3, 17 β HSD-8, 11 β HSD-1, U89717, CR1, AF0078850, HEP-27, or CR-3, a pharmaceutical agent for treatment of leukemia is provided by developing modulators for 17- β HSD-10 or Fvt-1 or a pharmaceutical agent for apoptosis regulation is provided by developing a modulator for 17 β HSD-10, U89717, SDR_SRL;
15 or for providing a pharmaceutical agent for affecting immune response by providing a modulator for AF016509, or providing a pharmaceutical agent for the treatment of cancer by providing modulators for AF016509, or providing a pharmaceutical agent for affecting cell growth by providing a modulator for U89717, or providing a pharmaceutical agent for the treatment of lung carcinoma by providing a modulator for SDR_SRL, or
20 providing a pharmaceutical agent for the regulation of inflammation or vasculitis by providing a modulator for DKFZ_ORF.

The SDR candidates detected according to the invention can be used particularly for the production of inhibitors, such as antibodies on protein level or antisense on nucleic acid level. Moreover, it is possible to provide diagnostics by using the SDR candidates detected according to the invention, e.g. in order to show a malfunction.

30 An important aspect of the present invention in view of the development of new drugs for the diagnosis and/or treatment of a disease is that the inventive approach aims on a target family, i.e. SDRs and not on a specific

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disease. This allows for the development of a number of drugs, which all influence the same target family. By this approach the amount of experiments, effort and money necessary to develop a new drug can be significantly reduced, since many results can be used parallel for further members of the same target family leading to further new drugs for different medical applications. Further this approach allows for affecting a target which is known or suspected to be highly relevant for a person's health. In contrast to the classical approach wherein starting from a disease a suitable target must be identified, this time and effort consuming procedure is not necessary with the inventive approach.

The invention is further elucidated by the following figures wherein

Fig. 1 represents the search engine for SDR candidates; The target sequence is compared to the specified core SDR motif, preferably in order from the N-terminus to the C-terminus.

Fig. 2 shows flow charts for the preferred implementation of the algorithm.
Fig. 2a shows a flow chart for data processing, while Fig. 2b shows a flow chart for the algorithm.

Fig. 3 depicts the development of pharmaceuticals on the basis of the SDR search according to the invention; The combination of virtual screening and classifying sequences to belong to the SDR family with the development of new drugs, as provided herein, is an efficient novel drug development strategy. By using the search results of the virtual SDR search new targets are obtained, from which drugs can be derived by various procedures.

Fig. 4 shows an alignment of human SDRs. 39 human SDR proteins were found in a database using the algorithm according to the invention. Throughout the various SDR proteins highly conserved amino acids

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are underlaid in grey. As can be seen from this figure the motifs selected for the algorithm of the invention are present in most of the human SDRs.

- 5 Tab. 1 Table 1 shows human and/or vertebrate SDRs detection with the algorithm according to the invention. The detected SDRs are also subject matter of this invention. Further, Table 1 includes an EST search for each SDR detected, with which the corresponding function and localization in tissue can be found or localized.
- 10
- 15 Tab.2 Table 2 shows mouse SDRs detected with the method according to the invention and the results of EST searches by using these mouse SDRs in human tissue. Thus using SDRs of various species, e.g. mammals, allows for localization and identification of new SDRs, in particular human SDRs on a genomic level. A preselection and/or identification of the SDR employed can be performed with the method according to the invention.
- 20
- 25 Tab. 3 Table 3 shows in bacterial SDRs which were detected with the method according to the invention. Such bacterial SDRs are particularly suitable for the development of novel antibiotics.
- 30 Tab. 4 Table 4 shows FabG_ proteins, i.e. an SDR subgroup. It is possible with the method according to the invention specifically identify desired subgroups by selection of further criteria in a second search step.
- Tab. 5 Table 5 shows SDRs from different fungi.

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Table 1: Human and/or vertebrates SDRs in non_redundant NCBI Database

Proteins or putative proteins not annotated SDRs

>gi|14035824|emb|CAC38508.1| unnamed protein product [Homo sapiens]

EST search:

Sequences producing significant alignments: (bits) Value

gi 12777652 emb AL514158.1 AL514158	AL514158 LTI_NFL006_PL2...	1865	0.0
gi 12791977 emb AL528484.1 AL528484	AL528484 LTI_NFL003_NBC...	1590	0.0
gi 10355379 gb BE893726.1 BE893726	601436638F1 NIH_MGC_72 H...	1178	0.0
gi 11984517 gb BF699109.1 BF699109	602126730F1 NIH_MGC_56 H...	1144	0.0
gi 10352047 gb BE892079.1 BE892079	601434975F1 NIH_MGC_72 H...	1126	0.0
gi 13577989 gb BG570336.1 BG570336	602590763F1 NIH_MGC_77 H...	1122	0.0
gi 13570346 gb BG562694.1 BG562694	602581487F1 NIH_MGC_76 H...	1104	0.0
gi 8156043 gb AW966207.1 AW966207	EST378280 MAGE resequence...	993	0.0
gi 13295675 gb BG402227.1 BG402227	602465788F1 NIH_MGC_75 H...	987	0.0
gi 6199963 gb AW152065.1 AW152065	xf74a01.x1 NCI_CGAP_Gas4 ...	918	0.0
gi 1967863 gb AA315514.1 AA315514	EST187305 Colon carcinoma...	831	0.0
gi 1957444 gb AA305116.1 AA305116	EST176117 Colon carcinoma...	831	0.0
gi 13332753 gb BG426247.1 BG426247	602492423F1 NIH_MGC_75 H...	797	0.0
gi 12346843 gb BF979524.1 BF979524	602288151F1 NIH_MGC_97 H...	789	0.0
gi 13573087 gb BG565434.1 BG565434	602583580F1 NIH_MGC_76 H...	743	0.0
gi 13339499 gb BG432993.1 BG432993	602495921F1 NIH_MGC_75 H...	733	0.0
gi 13966961 gb BG699051.1 BG699051	602678687F1 NIH_MGC_95 H...	720	0.0
gi 13336564 gb BG430058.1 BG430058	602499427F1 NIH_MGC_75 H...	712	0.0

>gi|14035828|emb|CAC38510.1| unnamed protein product [Homo sapiens]

EST Search:

Sequences producing significant alignments: (bits) Value

gi 12777652 emb AL514158.1 AL514158	AL514158 LTI_NFL006_PL2...	1865	0.0
gi 12791977 emb AL528484.1 AL528484	AL528484 LTI_NFL003_NBC...	1590	0.0
gi 13577989 gb BG570336.1 BG570336	602590763F1 NIH_MGC_77 H...	1197	0.0
gi 10355379 gb BE893726.1 BE893726	601436638F1 NIH_MGC_72 H...	1178	0.0
gi 10352047 gb BE892079.1 BE892079	601434975F1 NIH_MGC_72 H...	1156	0.0
gi 11984517 gb BF699109.1 BF699109	602126730F1 NIH_MGC_56 H...	1144	0.0
gi 6199963 gb AW152065.1 AW152065	xf74a01.x1 NCI_CGAP_Gas4 ...	1134	0.0
gi 13570346 gb BG562694.1 BG562694	602581487F1 NIH_MGC_76 H...	1104	0.0
gi 8156043 gb AW966207.1 AW966207	EST378280 MAGE resequence...	993	0.0
gi 13295675 gb BG402227.1 BG402227	602465788F1 NIH_MGC_75 H...	987	0.0
gi 13573087 gb BG565434.1 BG565434	602583580F1 NIH_MGC_76 H...	959	0.0
gi 13336564 gb BG430058.1 BG430058	602499427F1 NIH_MGC_75 H...	928	0.0
gi 10908030 db AV750182.1 AV750182	AV750182 NPC Homo sapie...	856	0.0
gi 1967863 gb AA315514.1 AA315514	EST187305 Colon carcinoma...	831	0.0
gi 1957444 gb AA305116.1 AA305116	EST176117 Colon carcinoma...	831	0.0
gi 13332753 gb BG426247.1 BG426247	602492423F1 NIH_MGC_75 H...	797	0.0
gi 12346843 gb BF979524.1 BF979524	602288151F1 NIH_MGC_97 H...	789	0.0
gi 13339499 gb BG432993.1 BG432993	602495921F1 NIH_MGC_75 H...	733	0.0
gi 13966961 gb BG699051.1 BG699051	602678687F1 NIH_MGC_95 H...	720	0.0

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>gi|14035944|emb|CAC38568.1| unnamed protein product [Homo sapiens]

EST search

Sequences producing significant alignments:	(bits)	Value
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gi 10964840 gb BF125800.1 BF125800	601763002F1 NIH_MGC_20 H...	866 0.0
gi 10718270 dbj AV701940.1 AV701940	AV701940 ADB Homo sapie...	835 0.0
gi 13987850 gb BG709476.1 BG709476	602674749F1 NIH_MGC_96 H...	765 0.0
gi 10370049 gb BE856729.1 BE856729	7f66h09.x1 Soares_NSF_F8...	724 0.0
gi 1523078 gb AA044874.1 AA044874	zk72b09.r1 Soares_pregnant...	720 0.0
gi 12102027 gb BF796973.1 BF796973	602258193F1 NIH_MGC_85 H...	712 0.0
gi 13180757 gb AA994212.1 AA994212	ou49b10.s1 NCI_CGAP_Br2 H...	680 0.0
gi 12672383 gb BG165680.1 BG165680	602345187F1 NIH_MGC_89 H...	670 0.0
gi 5394770 gb AI808204.1 AI808204	wf93f01.x1 Soares_NSF_F8...	640 0.0
gi 4334141 gb AI472051.1 AI472051	tj85e10.x1 Soares_NSF_F8...	626 e-177

>gi|14272510|emb|CAC39693.1| unnamed protein product [Homo sapiens]

EST search

Sequences producing significant alignments:	(bits)	Value
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gi 13523805 gb BG532267.1 BG532267	602561357F1 NIH_MGC_61 H...	1441 0.0
gi 13672847 gb BG621476.1 BG621476	602617846F1 NIH_MGC_79 H...	1425 0.0
gi 14046767 gb BG776463.1 BG776463	602663549F1 NIH_MGC_59 H...	1421 0.0
gi 13664977 gb BG613606.1 BG613606	602641959F1 NIH_MGC_61 H...	1421 0.0
gi 13584148 gb BG576495.1 BG576495	602598552F1 NIH_MGC_87 H...	1405 0.0
gi 13668653 gb BG617282.1 BG617282	602615306F1 NIH_MGC_76 H...	1370 0.0
gi 12892303 emb AL552940.1 AL552940	AL552940 LTI_NFL006_PL2...	1342 0.0
gi 13281485 gb BG388039.1 BG388039	602412885F1 NIH_MGC_92 H...	1334 0.0
gi 13574212 gb BG566559.1 BG566559	602585587F1 NIH_MGC_76 H...	1322 0.0
gi 13047273 gb BG290431.1 BG290431	602388279F1 NIH_MGC_93 H...	1316 0.0
gi 13672765 gb BG621394.1 BG621394	602617948F1 NIH_MGC_79 H...	1310 0.0
gi 13457137 gb BG495622.1 BG495622	602539957F1 NIH_MGC_59 H...	1279 0.0
gi 12945031 emb AL579716.1 AL579716	AL579716 LTI_FL012_TC1 ...	1215 0.0
gi 13458168 gb BG496651.1 BG496651	602537992F1 NIH_MGC_59 H...	1209 0.0
gi 12878925 emb AL546119.1 AL546119	AL546119 LTI_NFL006_PL2...	1187 0.0
gi 11111112 gb BF217526.1 BF217526	601885224F1 NIH_MGC_57 H...	1162 0.0
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gi 12417036 gb BG027942.1 BG027942	602294540F1 NIH_MGC_86 H...	1102 0.0
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gi 9777316 gb BE548671.1 BE548671	601074578F1 NIH_MGC_12 Ho...	1096 0.0
gi 11154063 gb BF240140.1 BF240140	601905643F1 NIH_MGC_54 H...	1092 0.0
gi 10889708 gb BF107182.1 BF107182	601824254F1 NIH_MGC_79 H...	1080 0.0
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gi 12937892 emb AL576092.1 AL576092	AL576092 LTI_NFL006_PL2...	1009 0.0
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gi 13527789 gb BG536244.1 BG536244	602565467F1 NIH_MGC_77 H...	1007 0.0
gi 12335519 gb BF968304.1 BF968304	602269321F1 NIH_MGC_84 H...	1003 0.0
gi 10201134 gb BE779936.1 BE779936	601467963F1 NIH_MGC_67 H...	993 0.0
gi 7948662 gb AW853145.1 AW853145	RC1-CT0249-200400-027-b02...	979 0.0
gi 7456666 gb AW664126.1 AW664126	hi04f06.x1 NCI_CGAP_GU1 H...	975 0.0
gi 12603373 gb BG109867.1 BG109867	602279533F1 NIH_MGC_86 H...	967 0.0

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gi|11941446|gb|BF667451.1|BF667451_602121811F1_NIH_MGC_56_H... 959 0.0
gi|12673375|gb|BG166672.1|BG166672_602339069F1_NIH_MGC_89_H... 955 0.0
gi|7949266|gb|AW853521.1|AW853521_RC1-CT0252-140300-026_g05... 940 0.0
gi|10584751|gb|BE971415.1|BE971415_601651403F1_NIH_MGC_81_H... 930 0.0
gi|2903664|gb|AA830565.1|AA830565_oc55a03.s1 NCI_CGAP_GCB1 ... 902 0.0
gi|6921588|gb|AW402833.1|AW402833_Ul-HF-BK0-aaq-e-07-0-Ul.r... 900 0.0
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>gi|14110766|gb|AAE57306.1| Sequence 2 from patent US 6171837

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 11081688 gb BF195132.1 BF195132_7n15f01.x1 NCI_CGAP_Brn2...	86	2e-14
gi 8908990 gb BE221672.1 BE221672_hu27e10.x1 NCI_CGAP_Mel15...	86	2e-14
gi 7703339 gb AW771285.1 AW771285_hn62d04.x1 NCI_CGAP_Kid11...	86	2e-14
gi 6661708 gb AW274678.1 AW274678_xv32d08.x1 SoaresNFL_T_G...	86	2e-14
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gi 5396293 gb AI809727.1 AI809727_wh77a07.x1 NCI_CGAP_CLL1 ...	86	2e-14
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gi 4264406 gb AI418475.1 AI418475_tf74h03.x1 NCI_CGAP_Brn23...	86	2e-14
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gi 2656640 gb AA680173.1 AA680173_zi11b06.s1 Soares_fetal_I...	86	2e-14
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gi 1728087 gb AA156462.1 AA156462_zl51h03.s1 Soares_pregnant...	86	2e-14
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gi 5592866 gb AI887702.1 AI887702_wm17d06.x1 NCI_CGAP_Ut4_H...	82	3e-13
gi 1891000 gb AA256871.1 AA256871_zr81f03.r1 Soares_NhHMPu...	82	3e-13
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>gi|14110767|gb|AAE57307.1| Sequence 3 from patent US 6171837

no DNA sequence available with acc # provided

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>gi|14110768|gb|AAE57308.1| Sequence 4 from patent US 6171837

no DNA sequence available with acc # provided

>gi|14110769|gb|AAE57309.1| Sequence 5 from patent US 6171837

no DNA sequence available with acc # provided

>gi|3994625|gb|AAC88053.1|AR010436 Sequence 1 from patent US 5756299

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 14178945 gb BG831358.1 BG831358 602766220F1 NIH_MGC_42 H...	1463	0.0
gi 14177680 gb BG830093.1 BG830093 602764845F1 NIH_MGC_42 H...	1463	0.0
gi 13404430 gb BG472244.1 BG472244 602513756F1 NIH_MGC_16 H...	1415	0.0
gi 14568476 gb BI117575.1 BI117575 602866754F1 NIH_MGC_7 Ho...	1392	0.0
gi 13982131 gb BG706614.1 BG706614 602674104F1 NIH_MGC_96 H...	1354	0.0
gi 13976241 gb BG703674.1 BG703674 602686647F1 NIH_MGC_95 H...	1342	0.0
gi 10390490 gb BE901372.1 BE901372 601674675F1 NIH_MGC_21 H...	1326	0.0
gi 12343809 gb BF976594.1 BF976594 602244271F1 NIH_MGC_48 H...	1300	0.0
gi 11641972 gb BF568592.1 BF568592 602184218F1 NIH_MGC_42 H...	1298	0.0
gi 11970704 gb BF685296.1 BF685296 602141648F1 NIH_MGC_46 H...	1279	0.0
gi 11252161 gb BF305282.1 BF305282 601892747F1 NIH_MGC_17 H...	1279	0.0
gi 11098442 gb BF204856.1 BF204856 601867158F1 NIH_MGC_17 H...	1275	0.0
gi 9137251 gb BE263706.1 BE263706 601192146F1 NIH_MGC_7 Hom...	1251	0.0
gi 10404479 gb BE909167.1 BE909167 601501782F1 NIH_MGC_70 H...	1249	0.0
gi 11151599 gb BF237681.1 BF237681 601841865F1 NIH_MGC_46 H...	1247	0.0
gi 9156256 gb BE281240.1 BE281240 601155341F1 NIH_MGC_21 Ho...	1247	0.0
gi 12342418 gb BF975203.1 BF975203 602244705F1 NIH_MGC_48 H...	1243	0.0
gi 14058856 gb BG748203.1 BG748203 602705827F1 NIH_MGC_43 H...	1235	0.0
gi 11263622 gb BF315274.1 BF315274 601902672F1 NIH_MGC_19 H...	1211	0.0
gi 11098117 gb BF204531.1 BF204531 601868138F1 NIH_MGC_17 H...	1211	0.0
gi 9133208 gb BE313377.1 BE313377 601147921F1 NIH_MGC_19 Ho...	1209	0.0
gi 12683322 gb BG176619.1 BG176619 602313206F1 NIH_MGC_85 H...	1207	0.0
gi 9882826 gb AV661812.1 AV661812 AV661812 GLC Homo sapien...	1205	0.0
gi 12615652 gb BG122143.1 BG122143 602349585F1 NIH_MGC_90 H...	1199	0.0
gi 11251336 gb BF304588.1 BF304588 601887980F1 NIH_MGC_17 H...	1174	0.0
gi 4536632 gb AI573258.1 AI573258 tn03e05.x1 NCI_CGAP_Bm25...	1170	0.0
gi 13032709 gb BG283133.1 BG283133 602406785F1 NIH_MGC_91 H...	1168	0.0
gi 10346623 gb BE889373.1 BE889373 601513264F1 NIH_MGC_71 H...	1162	0.0
gi 13137904 gb BG331552.1 BG331552 602433326F1 NIH_MGC_18 H...	1160	0.0
gi 8167102 gb AW975880.1 AW975880 EST387989 MAGE resequence...	1158	0.0
gi 9155643 gb BE280635.1 BE280635 601155778F1 NIH_MGC_21 Ho...	1156	0.0
gi 11258150 gb BF310575.1 BF310575 601895295F2 NIH_MGC_19 H...	1146	0.0
gi 8147508 gb AW957825.1 AW957825 EST369895 MAGE resequence...	1130	0.0
gi 13340715 gb BG434209.1 BG434209 602506154F1 NIH_MGC_79 H...	1114	0.0
gi 10216172 gb BE794974.1 BE794974 601589746F1 NIH_MGC_7 Ho...	1102	0.0
gi 11949082 gb BF675187.1 BF675187 602138110F1 NIH_MGC_83 H...	1088	0.0
gi 4194952 gb AI382182.1 AI382182 te70b01.x1 SoaresNFL_T_G...	1086	0.0
gi 8147585 gb AW957902.1 AW957902 EST369972 MAGE resequence...	1084	0.0
gi 14620169 gb BI160168.1 BI160168 602864026F1 NIH_MGC_42 H...	1076	0.0
gi 6588561 gb AW245568.1 AW245568 2822726.5prime NIH_MGC_7 ...	1076	0.0
gi 9137978 gb BE264422.1 BE264422 601191730F1 NIH_MGC_7 Hom...	1065	0.0
gi 6588571 gb AW245578.1 AW245578 2822726.3prime NIH_MGC_7 ...	1061	0.0

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gi|11617689|gb|BF530338.1|BF530338 602071618F1 NCI_CGAP_Brn... 1055 0.0
gi|14320386|gb|BG925863.1|BG925863 HNC21-1-B11.R HNC (Human... 1053 0.0
gi|2726589|gb|AA714315.1|AA714315 nw06c05.s1 NCI_CGAP_SS1 H... 1015 0.0
gi|2537901|gb|AA625514.1|AA625514 af72e06.r1 Soares_NhHMPu... 1007 0.0
gi|2155441|gb|AA442766.1|AA442766 zv60c08.s1 Soares_testis... 1007 0.0
gi|2464707|gb|AA613669.1|AA613669 no39h10.s1 NCI_CGAP_Pr23 ... 997 0.0
gi|13137575|gb|BG331137.1|BG331137 602431839F1 NIH_MGC_18 H... 993 0.0
gi|1211129|gb|N63300.1|N63300 yy71a11.s1 Soares_multiple_sc... 993 0.0
gi|1148734|gb|N30214.1|N30214 yw83h09.s1 Soares_placenta_8t... 989 0.0
gi|9866354|gb|AV645340.1|AV645340 AV645340 GLA Homo sapien... 983 0.0
gi|12412330|gb|BG025585.1|BG025585 602274505F1 NIH_MGC_85 H... 981 0.0
gi|3230271|gb|AI015935.1|AI015935 ov26c11.x1 Soares_testis... 977 0.0
gi|9882981|gb|AV661967.1|AV661967 AV661967 GLC Homo sapien... 975 0.0
gi|6399823|gb|AW168298.1|AW168298 xg62g11.x1 NCI_CGAP_Ut4 H... 969 0.0
gi|3840076|gb|AI244679.1|AI244679 qj97c09.x1 NCI_CGAP_Kid3 ... 969 0.0
gi|2243999|gb|AA507560.1|AA507560 ng88h09.s1 NCI_CGAP_Pr6 H... 965 0.0
gi|14058983|gb|BG748330.1|BG748330 602706579F1 NIH_MGC_43 H... 963 0.0
gi|5838015|gb|AI991112.1|AI991112 wu38c07.x1 Soares_Dieckgr... 954 0.0
gi|10216094|gb|BE794896.1|BE794896 601589638F1 NIH_MGC_7 Ho... 948 0.0
gi|9140017|gb|BE266440.1|BE266440 601193195F1 NIH_MGC_7 Hom... 938 0.0
gi|1210879|gb|N63050.1|N63050 yy70g11.s1 Soares_multiple_sc... 926 0.0
gi|8750451|gb|BE207053.1|BE207053 ba09d08.y1 NIH_MGC_7 Homo... 920 0.0
gi|5395010|gb|AI808444.1|AI808444 wf94h12.x1 Soares_NSF_F8... 918 0.0
gi|10813709|gb|AV716557.1|AV716557 AV716557 DCB Homo sapie... 914 0.0
gi|2883312|gb|AA813327.1|AA813327 ai81a07.s1 Soares_testis... 908 0.0
gi|10144813|gb|BE730821.1|BE730821 601570791F1 NIH_MGC_21 H... 906 0.0
gi|1193558|gb|N52392.1|N52392 yv49g09.s1 Soares_fetal_liver... 898 0.0
gi|2138860|gb|AA433946.1|AA433946 zw52g09.s1 Soares_total_f... 888 0.0
gi|4489892|gb|AI557529.1|AI557529 pt2.1-06.D05.r tumor2 Hom... 884 0.0
gi|12431844|gb|BG036553.1|BG036553 602326326F1 NIH_MGC_91 H... 880 0.0
gi|2221812|gb|AA492250.1|AA492250 ng79d12.s1 NCI_CGAP_Pr6 H... 876 0.0
gi|3803259|gb|AI221056.1|AI221056 qq09c12.x1 Soares_placent... 874 0.0
gi|3422302|gb|AI083879.1|AI083879 qf22c05.x1 NCI_CGAP_Brn25... 874 0.0
gi|11955171|gb|BF681276.1|BF681276 602155535F1 NIH_MGC_83 H... 872 0.0
gi|5591001|gb|AI885837.1|AI885837 wl62c01.x1 NCI_CGAP_Brn25... 866 0.0
gi|2159247|gb|AA446582.1|AA446582 zw84d08.s1 Soares_total_f... 862 0.0
gi|2341742|gb|AA568688.1|AA568688 nm06f08.s1 NCI_CGAP_Co10 ... 856 0.0
gi|4833888|gb|AI669114.1|AI669114 wb80e10.x1 NCI_CGAP_Pr28 ... 854 0.0
gi|10293455|gb|AV691592.1|AV691592 AV691592 GKC Homo sapie... 839 0.0
gi|3988221|gb|AI304532.1|AI304532 qo55a06.x1 NCI_CGAP_Co8 H... 833 0.0
gi|2731990|gb|AA720021.1|AA720021 zh22e05.s1 Soares_pineal... 831 0.0
gi|1965893|gb|AA313563.1|AA313563 EST185441 Colon carcinoma... 831 0.0
gi|7316134|gb|AW615416.1|AW615416 ba09d08.x1 NIH_MGC_7 Homo... 821 0.0
gi|9875231|gb|AV654217.1|AV654217 AV654217 GLC Homo sapien... 815 0.0
gi|4489893|gb|AI557530.1|AI557530 pt2.1-06.D05b.r tumor2 Ho... 811 0.0
gi|4598919|gb|AI589871.1|AI589871 tm81d01.x1 NCI_CGAP_Brn25... 803 0.0

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>gi|3994626|gb|AAC88054.1|AR010437 Sequence 3 from patent US 5756299
no DNA sequence available with acc # provided

>gi|3994627|gb|AAC88055.1|AR010438 Sequence 4 from patent US 5756299
no DNA sequence available with acc # provided

>gi|3994628|gb|AAC88056.1|AR010439 Sequence 5 from patent US 5756299
no DNA sequence available with acc # provided

>gi|10049861|gb|AAE26768.1| Sequence 1 from patent US 5952209

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 10850515 dbj AV732970.1 AV732970 AV732970 cdA Homo sapie...	80	2e-12
gi 14051966 gb BG741313.1 BG741313 602634450F1 NCI_CGAP_Skn...	78	8e-12
gi 14051796 gb BG741143.1 BG741143 602631813F1 NCI_CGAP_Skn...	78	8e-12
gi 8158534 gb AW968693.1 AW968693 EST380769 MAGE resequence...	78	8e-12
gi 7846487 gb AW794617.1 AW794617 RC6-UM0014-290300-013-A08...	78	8e-12
gi 6924798 gb AW405741.1 AW405741 UI-HF-BL0-abv-g-11-0-UI.r...	78	8e-12
gi 6463032 gb AW188672.1 AW188672 xk02a07.x1 NCI_CGAP_Co18 ...	78	8e-12
gi 2458420 gb AA609992.1 AA609992 af18a10.s1 Soares_testis_...	78	8e-12
gi 2210648 gb AA481096.1 AA481096 aa29b12.r1 NCI_CGAP_GCB1 ...	78	8e-12
gi 1957157 gb AA304808.1 AA304808 EST175827 Monocytes, stim...	78	8e-12
gi 1291544 gb W17165.1 W17165 zb12g01.r1 Soares_fetal_lung_...	78	8e-12
gi 11594354 gb BF511056.1 BF511056 UI-H-BI4-apl-h-02-0-UI.s...	76	3e-11
gi 7280943 gb AW593685.1 AW593685 xl97h06.x1 NCI_CGAP_Ut1 H...	76	3e-11
gi 7246189 gb AW574650.1 AW574650 UI-HF-BL0-abv-g-11-0-UI.s...	76	3e-11
gi 6652091 gb AW059769.1 AW059769 LE4e05.yg DNC15 Homo sapi...	76	3e-11
gi 5809845 gb AI982593.1 AI982593 wt53b01.x1 NCI_CGAP_Pan1 ...	76	3e-11
gi 5803948 gb AI978918.1 AI978918 wr61h01.x1 NCI_CGAP_Ut1 H...	76	3e-11
gi 4457857 gb AI540484.1 AI540484 tq24e12.x1 NCI_CGAP_Ut1 H...	76	3e-11
gi 4110322 gb AI358701.1 AI358701 qx14a10.x1 NCI_CGAP_Lym12...	76	3e-11
gi 2563996 gb AA640217.1 AA640217 03 subtracted 3' EST libr...	76	3e-11
gi 2457366 gb AA608938.1 AA608938 af03f01.s1 Soares_testis_...	76	3e-11
gi 2210593 gb AA481041.1 AA481041 aa29b12.s1 NCI_CGAP_GCB1 ...	76	3e-11
gi 1934027 gb AA287021.1 AA287021 zs57c03.s1 NCI_CGAP_GCB1 ...	76	3e-11

>gi|10049862|gb|AAE26769.1| Sequence 3 from patent US 5952209

no DNA sequence available with acc # provided

>gi|5942061|gb|AAE01593.1| Sequence 1 from patent US 5858750

no DNA sequence available with acc # provided

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>gi|5942061|gb|AAE01593.1| Sequence 1 from patent US 5858750

no DNA sequence available with acc # provided

>gi|5942062|gb|AAE01594.1| Sequence 3 from patent US 5858750

no DNA sequence available with acc # provided

>gi|14272566|emb|CAC39721.1| unnamed protein product [Homo sapiens]

EST Search

Sequences producing significant alignments: (bits) Value

gi 14169716 gb BG822129.1 BG822129	602726271F1 NIH_MGC_15 H...	1518	0.0
gi 14568272 gb BI117371.1 BI117371	602867919F1 NIH_MGC_7 Ho...	1451	0.0
gi 9803527 gb BE559808.1 BE559808	601346972F1 NIH_MGC_8 Hom...	1404	0.0
gi 10150139 gb BE736147.1 BE736147	601307226F1 NIH_MGC_39 H...	1380	0.0
gi 12041329 gb BF725418.1 BF725418	bx15f11.y1 Human_Iris cD...	1300	0.0
gi 5545428 gb AI871379.1 AI871379	wi81d08.x1 NCI_CGAP_Brn25...	1298	0.0
gi 101627791 gb BE748799.1 BE748799	601572007T1 NIH_MGC_55 H...	1296	0.0
gi 10162316 gb BE748324.1 BE748324	601572007F1 NIH_MGC_55 H...	1255	0.0
gi 12758392 gb BG248576.1 BG248576	602400744F1 NIH_MGC_15 H...	1201	0.0
gi 11251209 gb BF304472.1 BF304472	601887831F1 NIH_MGC_17 H...	1197	0.0
gi 9803869 gb BE560051.1 BE560051	601347483F1 NIH_MGC_8 Hom...	1197	0.0
gi 12670294 gb BG163591.1 BG163591	602338741F1 NIH_MGC_89 H...	1191	0.0
gi 5178261 gb AI762594.1 AI762594	wi56b09.x1 NCI_CGAP_Co16 ...	1185	0.0
gi 9122527 gb BE252388.1 BE252388	601117771F1 NIH_MGC_16 Ho...	1170	0.0
gi 14620762 gb BI160761.1 BI160761	602864839F1 NIH_MGC_42 H...	1148	0.0
gi 6709871 gb AW300271.1 AW300271	xs58h07.x1 NCI_CGAP_Kid11...	1144	0.0
gi 14057456 gb BG746803.1 BG746803	602704139F1 NIH_MGC_15 H...	1132	0.0
gi 5108921 gb AI740633.1 AI740633	wg23g01.x1 Soares_NSF_F8 ...	1090	0.0
gi 13343784 gb BG437278.1 BG437278	602490558F1 NIH_MGC_18 H...	1068	0.0
gi 6570140 gb AW237763.1 AW237763	xm81b04.x1 NCI_CGAP_Kid11...	1059	0.0
gi 4372796 gb AI479628.1 AI479628	tm32d07.x1 NCI_CGAP_CLL1 ...	1051	0.0
gi 5540213 gb AI867197.1 AI867197	wa01c10.x1 NCI_CGAP_Kid11...	1045	0.0
gi 13792425 gb BG655016.1 BG655016	ib44h01.y1 HR85 islet Ho...	1041	0.0
gi 11448154 gb BF435839.1 BF435839	nab42e01.x1 Soares_NSF_F...	1035	0.0
gi 10938383 gb BF108693.1 BF108693	7i44e02.x1 Soares_NSF_F8...	1033	0.0
gi 8169897 gb AW978626.1 AW978626	EST390735 MAGE resequence...	1031	0.0
gi 10036058 gb BE675517.1 BE675517	7f10f02.x1 NCI_CGAP_CLL1 ...	1013	0.0
gi 5933828 gb AW058189.1 AW058189	wv83h01.x1 Soares_thymus_...	1011	0.0
gi 4190356 gb AI380503.1 AI380503	tf95d02.x1 NCI_CGAP_CLL1 ...	1007	0.0
gi 5113008 gb AI744631.1 AI744631	wg04g09.x1 Soares_NSF_F8 ...	1005	0.0
gi 5450901 gb AI830241.1 AI830241	wj78h11.x1 NCI_CGAP_Lu19 ...	1003	0.0
gi 4598007 gb AI588959.1 AI588959	tk15d10.x1 Soares_NhHMPu ...	999	0.0
gi 9970354 gb BE646054.1 BE646054	7e92d04.x1 NCI_CGAP_CLL1 ...	995	0.0
gi 5232040 gb AI765531.1 AI765531	wi81b11.x1 NCI_CGAP_Kid12...	973	0.0
gi 4113265 gb AI361644.1 AI361644	qy86d07.x1 NCI_CGAP_Brn25...	971	0.0
gi 11082796 gb BF195666.1 BF195666	7n86g02.x1 NCI_CGAP_Ov18...	961	0.0
gi 11682572 gb BF590248.1 BF590248	nab22a02.x1 Soares_NSF_F...	957	0.0
gi 4311958 gb AI457940.1 AI457940	tj55h09.x1 Soares_NSF_F8 ...	957	0.0
gi 6710832 gb AW301155.1 AW301155	xs57a11.x1 NCI_CGAP_Kid11...	950	0.0
gi 5663387 gb AI927423.1 AI927423	wo75e11.x1 NCI_CGAP_Pr22 ...	950	0.0
gi 5766733 gb AI969915.1 AI969915	wq77e03.x1 NCI_CGAP_Pr28 ...	948	0.0
gi 2463985 gb AA612947.1 AA612947	nq38e11.s1 NCI_CGAP_Co10 ...	948	0.0
gi 5664220 gb AI928256.1 AI928256	wo67a08.x1 NCI_CGAP_Pr22 ...	946	0.0
gi 6746198 gb AW316942.1 AW316942	xw13a08.x1 NCI_CGAP_Brn53...	934	0.0
gi 1377082 gb W68057.1 W68057	zd42h12.r1 Soares_fetal heart...	930	0.0
gi 1959057 gb AA306658.1 AA306658	EST177664 Jurkat T-cells ...	918	0.0
gi 5660470 gb AI924506.1 AI924506	wn61a01.x1 NCI_CGAP_Lu19 ...	912	0.0
gi 3095277 gb AA937166.1 AA937166	ok13a08.s1 Soares_NSF_F8 ...	908	0.0
gi 2986172 gb AA877095.1 AA877095	ob09d05.s1 NCI_CGAP_Kid3 ...	900	0.0

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>gi|5942062|gb|AAE01594.1| Sequence 3 from patent US 5858750

No cDNA sequence available with accession # provided

>gi|12821846|gb|AAE48287.1| Sequence 2 from patent US 6106829

No cDNA sequence available with accession # provided

>gi|11340737|emb|CAC17063.1| unnamed protein product [Homo sapiens]

EST search

Sequences producing significant alignments: (bits) Value

gi 13401922 gb BG469647.1 BG469647	602534103F1 NIH_MGC_15 H...	1550	0.0
gi 13746560 gb BG220539.1 BG220539	RST40325 Athersys RAGE L...	1483	0.0
gi 13963233 gb BG697241.1 BG697241	602660481F1 NCI_CGAP_Skn...	1463	0.0
gi 14053553 gb BG742900.1 BG742900	602632481F1 NCI_CGAP_Skn...	1457	0.0
gi 13967002 gb BG699072.1 BG699072	602678713F1 NIH_MGC_95 H...	1439	0.0
gi 14053781 gb BG743128.1 BG743128	602634270F1 NCI_CGAP_Skn...	1427	0.0
gi 13410718 gb BG478523.1 BG478523	602524002F1 NIH_MGC_20 H...	1419	0.0
gi 14064290 gb BG753637.1 BG753637	602732827F1 NIH_MGC_43 H...	1409	0.0
gi 9146489 gb BE272160.1 BE272160	601141656F1 NIH_MGC_9 Hom...	1409	0.0
gi 14047524 gb BG777207.1 BG777207	602664432F1 NIH_MGC_59 H...	1402	0.0
gi 14651659 gb BI196639.1 BI196639	602755427F1 NIH_MGC_19 H...	1388	0.0
gi 14059064 gb BG748411.1 BG748411	602705974F1 NIH_MGC_43 H...	1380	0.0
gi 13336094 gb BG429588.1 BG429588	602501268F1 NIH_MGC_75 H...	1368	0.0
gi 9124275 gb BE253854.1 BE253854	601112818F1 NIH_MGC_16 Ho...	1364	0.0
gi 12604238 gb BG110732.1 BG110732	602279029F1 NIH_MGC_86 H...	1358	0.0
gi 12607924 gb BG114418.1 BG114418	602285710F1 NIH_MGC_86 H...	1348	0.0
gi 13527202 gb BG535657.1 BG535657	602563366F1 NIH_MGC_77 H...	1344	0.0
gi 13289966 gb BG396518.1 BG396518	602459353F1 NIH_MGC_16 H...	1342	0.0
gi 10399800 gb BE906369.1 BE906369	601498517F1 NIH_MGC_70 H...	1340	0.0
gi 10156435 gb BE742443.1 BE742443	601575210F1 NIH_MGC_9 Ho...	1330	0.0
gi 6361758 gb AI305108.1 AI305108	HA2404 Human fetal liver ...	1316	0.0
gi 13570738 gb BG563086.1 BG563086	602581878F1 NIH_MGC_76 H...	1314	0.0
gi 14565107 gb BI114206.1 BI114206	602862564F1 NIH_MGC_17 H...	1302	0.0
gi 14566335 gb BI115434.1 BI115434	602863311F1 NIH_MGC_17 H...	1296	0.0
gi 6359266 gb AI064994.1 AI064994	HA0821 Human fetal liver ...	1296	0.0
gi 9186637 gb BE302889.1 BE302889	ba70g10.y1 NIH_MGC_20 Hom...	1289	0.0
gi 14566302 gb BI115401.1 BI115401	602863260F1 NIH_MGC_17 H...	1279	0.0
gi 4763039 gb AI659469.1 AI659469	tu30g07.x1 NCI_CGAP_Pr28 ...	1271	0.0
gi 9328145 gb BE382780.1 BE382780	601298459F1 NIH_MGC_19 Ho...	1259	0.0
gi 10160188 gb BE746196.1 BE746196	601578644F1 NIH_MGC_9 Ho...	1253	0.0
gi 13459320 gb BG497803.1 BG497803	602543080F1 NIH_MGC_60 H...	1251	0.0
gi 12761697 gb BG251881.1 BG251881	602364502F1 NIH_MGC_90 H...	1251	0.0
gi 13999085 gb BG719898.1 BG719898	602691430F1 NIH_MGC_97 H...	1247	0.0
gi 13969001 gb BG700048.1 BG700048	602681055F1 NIH_MGC_95 H...	1241	0.0
gi 12678524 gb BG171821.1 BG171821	602322603F1 NIH_MGC_89 H...	1237	0.0
gi 9179232 gb BE295680.1 BE295680	601175688F1 NIH_MGC_17 Ho...	1235	0.0
gi 13523981 gb BG532442.1 BG532442	602561968F1 NIH_MGC_61 H...	1227	0.0
gi 13406852 gb BG474575.1 BG474575	602517363F1 NIH_MGC_16 H...	1227	0.0

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gi|12609069|gb|BG115563.1|BG115563 602317253F1 NIH_MGC_88 H... 1213 0.0
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gi|12770117|gb|BG260301.1|BG260301 602371417F1 NIH_MGC_93 H... 1203 0.0
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gi|9323581|gb|BE378216.1|BE378216 601237991F1 NIH_MGC_44 Ho... 1199 0.0
gi|14471561|gb|BI064034.1|BI064034 IL3-UT0119-120401-430-G0... 1197 0.0
gi|9722042|gb|BE514828.1|BE514828 601316764F1 NIH_MGC_9 Hom... 1191 0.0
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gi|11952823|gb|BF678928.1|BF678928 602153555F1 NIH_MGC_83 H... 1183 0.0
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gi|12687397|gb|BG180694.1|BG180694 602329481F1 NIH_MGC_91 H... 1142 0.0
gi|11953928|gb|BF680033.1|BF680033 602154752F1 NIH_MGC_83 H... 1132 0.0
gi|13458797|gb|BG497280.1|BG497280 602537844F1 NIH_MGC_59 H... 1128 0.0
gi|9179583|gb|BE296026.1|BE296026 601175058F1 NIH_MGC_17 Ho... 1128 0.0
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gi|10348906|gb|BE890514.1|BE890514 601431585F1 NIH_MGC_72 H... 1037 0.0

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gi|14471659|gb|BI064132.1|BI064132 IL3-UT0119-170401-459-H0... 1025 0.0
gi|7280592|gb|AW593334.1|AW593334 hg13d03.x1 SoaresNFL_T_G... 1023 0.0
gi|10587293|gb|BE973957.1|BE973957 601680275F1 NIH_MGC_83 H... 1021 0.0
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>gi|10045089|emb|CAC07797.1| unnamed protein product [unidentified]

EST search:

Sequences producing significant alignments: (bits) Value

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gi|10949847|dbj|AU125131.1|AU125131 AU125131 NT2RM4 Homo sa... 1471 0.0
gi|10992681|dbj|AU132327.1|AU132327 AU132327 NT2RP3 Homo sa... 1453 0.0
gi|3214525|gb|AI005015.1|AI005015 ou91a01.x1 NCI_CGAP_Kid3 ... 1451 0.0
gi|3674126|gb|AI146444.1|AI146444 qb93a03.x1 Soares_fetal_h... 1425 0.0
gi|3412550|gb|AI078142.1|AI078142 oz30b04.x1 Soares_total_f... 1417 0.0
gi|13721603|gb|BG199916.1|BG199916 RST19212 Athersys RAGE L... 1413 0.0
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gi|10991451|dbj|AU131097.1|AU131097 AU131097 NT2RP3 Homo sa... 1390 0.0
gi|10991758|dbj|AU131404.1|AU131404 AU131404 NT2RP3 Homo sa... 1362 0.0
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gi|11004302|dbj|AU142781.1|AU142781 AU142781 Y79AA1 Homo sa... 1344 0.0
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gi|10996985|dbj|AU136446.1|AU136446 AU136446 PLACE1 Homo sa... 1336 0.0
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gi|11264224|gb|BF315938.1|BF315938 601895882F1 NIH_MGC_19 H... 1247 0.0
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gi|10098245|gb|BE710071.1|BE710071 IL3-HT0618-030800-233-G0... 1209 0.0
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gi|13704200|gb|BG182513.1|BG182513 RST1389 Athersys RAGE Li... 1191 0.0
gi|11283822|gb|BF337571.1|BF337571 602035323F1 NCI_CGAP_Brn... 1191 0.0
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 gi|5393220|gb|AI806654.1|AI806654_wf35b04.x1 Soares_NFL_T_G... 1168 0.0
 gi|12101942|gb|BF796888.1|BF796888_602258274F1 NIH_MGC_85 H... 1166 0.0
 gi|10965228|gb|BF126270.1|BF126270_601650451F1 NIH_MGC_76 H... 1154 0.0
 gi|11968943|gb|BF683535.1|BF683535_602139737F1 NIH_MGC_46 H... 1144 0.0
 gi|2992678|gb|AA883079.1|AA883079_am24a03.s1 Soares_NFL_T_G... 1138 0.0
 gi|10823746|dbj|AV721848.1|AV721848_AV721848 HTB Homo sapie... 1136 0.0
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 gi|10951089|dbj|AU126373.1|AU126373 AU126373 NT2RP1 Homo sa... 1132 0.0
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 gi|13050584|gb|BG292110.1|BG292110_602386409F1 NIH_MGC_93 H... 1126 0.0
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 gi|4073310|gb|AI336383.1|AI336383_qt51c08.x1 Soares_fetal_I... 940 0.0

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>gi|14598964|emb|CAC43882.1| 21676 ADH [Homo sapiens]

EST Search:

Organ: skin

Organ: kidney

Tissue type: renal cell adenocarcinoma

Organ: lung

Tissue type: small cell carcinoma

Organ: testis

Organ: skin

Tissue type: melanotic melanoma

Sequences producing significant alignments: (bits) Value

gi 14052242 gb BG741589.1 BG741589	602635416F1 NCI_CGAP_Skn...	1559	0.0
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gi 12347068 gb BF979853.1 BF979853	602288368T1 NIH_MGC_97 H...	1285	0.0
gi 13031288 gb BG282361.1 BG282361	602402863F1 NIH_MGC_20 H...	1283	0.0
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gi 12335074 gb BF967768.1 BF967768	602287657T1 NIH_MGC_96 H...	1203	0.0
gi 10358131 gb BE895089.1 BE895089	601436007F1 NIH_MGC_72 H...	1183	0.0
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gi 12904138 emb AL559036.1 AL559036	AL559036_LT1NFL008_TC2...	1124	0.0
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gi 12727118 gb BG231973.1 BG231973	naf34g12.x1 Soares_NPBMC...	1058	0.0
gi 5848488 gb AW001572.1 AW001572	wu34f05.x1 Soares_Dieckgr...	1012	0.0
gi 11764835 gb BE962188.2 BE962188	601655404R1 NIH_MGC_65 H...	1000	0.0
gi 14818515 gb BI260323.1 BI260323	602969342F1 NIH_MGC_12 H...	994	0.0
gi 9186562 gb BE302814.1 BE302814	ba69c04.y1 NIH_MGC_20 Hom...	988	0.0
gi 1365172 gb W58459.1 W58459	zd25h06.s1 Soares_fetal_heart...	972	0.0
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gi 1365130 gb W58347.1 W58347	zd25b06.s1 Soares_fetal_heart...	958	0.0
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gi 9340527 gb BE395162.1 BE395162	601309505F1 NIH_MGC_44 Ho...	931	0.0
gi 1365185 gb W58472.1 W58472	zd25b06.r1 Soares_fetal_heart...	931	0.0
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gi 4853165 gb AI673434.1 AI673434	wf19a10.x1 Soares_Dieckgr...	911	0.0
gi 9340769 gb BE395404.1 BE395404	601309913F1 NIH_MGC_44 Ho...	905	0.0
gi 6133237 gb AW131630.1 AW131630	xf32d02.x1 NCI_CGAP_Bm50...	903	0.0
gi 5912902 gb AW050632.1 AW050632	wz19e08.x1 Soares_Dieckgr...	885	0.0
gi 4187886 gb AI378033.1 AI378033	te67g09.x1 SoaresNFL_T_G...	877	0.0
gi 1365227 gb W58514.1 W58514	zd25h06.r1 Soares_fetal_heart...	871	0.0
gi 3048078 gb AA908673.1 AA908673	ol04d06.s1 NCI_CGAP_Lu5 H...	857	0.0
gi 13520318 gb BG528781.1 BG528781	602580128F1 NIH_MGC_60 H...	853	0.0
gi 3598437 gb AI129923.1 AI129923	qc41d08.x1 Soares_pregnan...	847	0.0
gi 3778197 gb AI214596.1 AI214596	qm28h07.x1 NCI_CGAP_Lu5 H...	837	0.0
gi 2161847 gb AA448177.1 AA448177	zw83b12.s1 Soares_testis ...	833	0.0
gi 6992857 gb AW452081.1 AW452081	UI-H-BI3-aln-c-06-0-UI.s1...	825	0.0
gi 13996787 gb BG717600.1 BG717600	602698216F1 NIH_MGC_97 H...	787	0.0
gi 3752620 gb AI200014.1 AI200014	qf90d03.x1 Soares_placent...	762	0.0
gi 2350443 gb AA575928.1 AA575928	nm56b12.s1 NCI_CGAP_Br3 H...	760	0.0
gi 4629290 gb AI620164.1 AI620164	tu46c12.x1 NCI_CGAP_Pr28 ...	756	0.0
gi 14385896 gb BG983161.1 BG983161	IL5-CN0068-060301-381-h0...	754	0.0

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gi|2879112|gb|AA809706.1|AA809706 nk96f06.s1 NCI_CGAP_Co3 H... 738 0.0
gi|3803861|gb|AI221658.1|AI221658 qg93d04.x1 SoaresNFL_T_G... 712 0.0

>gi|14598968|emb|CAC43884.1| 21615 ADH [Homo sapiens]

EST Search:

Organ: brain

Tissue type: neuroblastoma cells

Tissue type: placenta

Tissue type: placenta

Sex: male

Organ: brain

Tissue type: neuroblastoma cells

Sequences producing significant alignments:

(bits) Value

gi 12786589 emb AL523096.1 AL523096 AL523096 LTI_NFL003_NBC...	1707	0.0
gi 12889983 emb AL551741.1 AL551741 AL551741 LTI_NFL006_PL2...	1653	0.0
gi 12936195 emb AL575230.1 AL575230 AL575230 LTI_NFL006_PL2...	1487	0.0
gi 12793625 emb AL530132.1 AL530132 AL530132 LTI_NFL001_NBC...	1457	0.0
gi 13294054 gb BG400606.1 BG400606 602464263F1 NIH_MGC_75 H...	1443	0.0
gi 13452667 gb BG491155.1 BG491155 602518792F1 NIH_MGC_18 H...	1401	0.0
gi 13982652 gb BG706873.1 BG706873 602672037F1 NIH_MGC_96 H...	1387	0.0
gi 3281013 gb AI041819.1 AI041819 oy34a10.x1 Soares_parathy...	1352	0.0
gi 12793624 emb AL530131.1 AL530131 AL530131 LTI_NFL001_NBC...	1346	0.0
gi 13545674 gb BG547009.1 BG547009 602573805F1 NIH_MGC_77 H...	1340	0.0
gi 13976480 gb BG703780.1 BG703780 602686804F1 NIH_MGC_95 H...	1338	0.0
gi 14051133 gb BG740480.1 BG740480 602633875F1 NCI_CGAP_Skn...	1330	0.0
gi 13039621 gb BG286600.1 BG286600 602381608F1 NIH_MGC_93 H...	1314	0.0
gi 11257955 gb BF310393.1 BF310393 601895043F1 NIH_MGC_19 H...	1304	0.0
gi 2839375 gb AA780044.1 AA780044 zj24e12.s1 Soares_fetal...	1302	0.0
gi 11265005 gb BF316648.1 BF316648 601903206F1 NIH_MGC_19 H...	1272	0.0
gi 8154981 gb AW965145.1 AW965145 EST377218 MAGE resequence...	1272	0.0
gi 3238050 gb AI022809.1 AI022809 cw55f02.x1 Soares_parathy...	1256	0.0
gi 13544541 gb BG545876.1 BG545876 602573161F1 NIH_MGC_77 H...	1238	0.0
gi 12598260 gb BG104418.1 BG104418 602311036F1 NIH_MGC_20 H...	1225	0.0
gi 12598014 gb BG104172.1 BG104172 602310736F1 NIH_MGC_20 H...	1221	0.0
gi 12606210 gb BG112704.1 BG112704 602282264F1 NIH_MGC_86 H...	1219	0.0
gi 2877836 gb AA808430.1 AA808430 oe53b08.s1 NCI_CGAP_Lu5 H...	1207	0.0
gi 4073201 gb AI336274.1 AI336274 qt45e02.x1 Soares_fetal...	1201	0.0
gi 6471396 gb AW192697.1 AW192697 xl48h04.x1 NCI_CGAP_Pan1 ...	1183	0.0
gi 9323894 gb BE378429.1 BE378429 601236767F1 NIH_MGC_44 Ho...	1151	0.0
gi 12910323 emb AL562168.1 AL562168 AL562168 LTI_NFL003_NBC...	1149	0.0
gi 9186202 gb BE302454.1 BE302454 ba65f04.y1 NIH_MGC_20_Hom...	1107	0.0
gi 9186195 gb BE302447.1 BE302447 ba65e04.y1 NIH_MGC_20_Hom...	1101	0.0
gi 5813571 gb AI986294.1 AI986294 wz64c08.x1 NCI_CGAP_Mel15...	1078	0.0
gi 4435368 gb AI521233.1 AI521233 to66f02.x1 NCI_CGAP_Gas4 ...	1076	0.0
gi 12875811 emb AL543333.1 AL543333 AL543333 LTI_NFL006_PL2...	1070	0.0
gi 5109073 gb AI740785.1 AI740785 wg24b10.x1 Soares_NSF_F8...	1056	0.0
gi 2993433 gb AA883903.1 AA883903 aj13a01.s1 Soares_parathy...	1056	0.0
gi 3400111 gb AI073467.1 AI073467 ov45a08.x1 Soares_testis ...	1048	0.0
gi 10350081 gb BE891095.1 BE891095 601432208F1 NIH_MGC_72 H...	1046	0.0
gi 6228615 gb AW157214.1 AW157214 au92h07.x1 Schneider_feta...	1038	0.0
gi 5858190 gb AW009412.1 AW009412 ws82c11.x1 NCI_CGAP_Co3 H...	1030	0.0
gi 2324986 gb AA554447.1 AA554447 nl14h10.s1 NCI_CGAP_Br2 H...	1028	0.0
gi 5546002 gb AI871953.1 AI871953 wm53h05.x1 NCI_CGAP_Ut2 H...	1024	0.0
gi 2955773 gb AA863294.1 AA863294 og93b12.s1 NCI_CGAP_Kid5 ...	1014	0.0
gi 2690528 gb AA689601.1 AA689601 nv66b12.s1 NCI_CGAP_GCB1 ...	1008	0.0
gi 13294752 gb BG401304.1 BG401304 602465415F1 NIH_MGC_75 H...	1006	0.0

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gi|4598887|gb|AI589839.1|AI589839 tm81a02.x1 NCI_CGAP_Brn25... 1006 0.0
 gi|4834180|gb|AI669406.1|AI669406 ty32b07.x1 NCI_CGAP_Ut2 H... 1002 0.0

>gi|14598962|emb|CAC43881.1| 33756 ADH [Homo sapiens]

EST Search:

Organ: brain
 Tissue type: anaplastic oligodendrogloma

Organ: colon
 Tissue type: colon tumor, RER+

Organ: kidney

Organ: colon
 Tissue type: adenocarcinoma cell line

Sequences producing significant alignments: (bits) Value

gi 5545428 gb AI871379.1 AI871379 wl81d08.x1 NCI_CGAP_Brn25...	1291	0.0
gi 5178261 gb AI762594.1 AI762594 wi56b09.x1 NCI_CGAP_Co16 ...	1193	0.0
gi 6709871 gb AW300271.1 AW300271 xs58h07.x1 NCI_CGAP_Kid11...	1136	0.0
gi 5108921 gb AI740633.1 AI740633 wg23g01.x1 Soares_NSF_F8...	1067	0.0
gi 14169716 gb BG822129.1 BG822129 602726271F1 NIH_MGC_15 H...	1061	0.0
gi 6570140 gb AW237763.1 AW237763 xm81b04.x1 NCI_CGAP_Kid11...	1051	0.0
gi 10938383 gb BF108693.1 BF108693 7144e02.x1 Soares_NSF_F8...	1025	0.0
gi 5540213 gb AI867197.1 AI867197 wa01c10.x1 NCI_CGAP_Kid11...	1021	0.0
gi 11448154 gb BF435839.1 BF435839 nab42e01.x1 Soares_NSF_F...	1011	0.0
gi 5933828 gb AW058189.1 AW058189 wv83h01.x1 Soares_thymus...	1003	0.0
gi 4190356 gb AI380503.1 AI380503 tf95d02.x1 NCI_CGAP_CLL1 ...	999	0.0
gi 5450901 gb AI830241.1 AI830241 wj78h11.x1 NCI_CGAP_Lu19 ...	995	0.0
gi 5113008 gb AI744631.1 AI744631 wg04g09.x1 Soares_NSF_F8...	981	0.0
gi 4598007 gb AI588959.1 AI588959 tk15d10.x1 Soares_NhHMPu...	975	0.0
gi 11682572 gb BF590248.1 BF590248 nab22a02.x1 Soares_NSF_F...	950	0.0
gi 5232040 gb AI765531.1 AI765531 wi81b11.x1 NCI_CGAP_Kid12...	950	0.0
gi 4311958 gb AI457940.1 AI457940 tj55h09.x1 Soares_NSF_F8...	950	0.0
gi 6710832 gb AW301155.1 AW301155 xs57a11.x1 NCI_CGAP_Kid11...	942	0.0
gi 5664220 gb AI928256.1 AI928256 wo67a08.x1 NCI_CGAP_Pr22 ...	938	0.0
gi 6746198 gb AW316942.1 AW316942 xw13a08.x1 NCI_CGAP_Brn53...	926	0.0
gi 5663387 gb AI927423.1 AI927423 wo75e11.x1 NCI_CGAP_Pr22 ...	926	0.0
gi 5766733 gb AI969915.1 AI969915 wq77e03.x1 NCI_CGAP_Pr28 ...	924	0.0
gi 9803527 gb BE559808.1 BE559808 601346972F1 NIH_MGC_8 Hom...	918	0.0
gi 10819930 gb BF061020.1 BF061020 7j62f12.x1 Soares_NSF_F8...	890	0.0
gi 3095277 gb AA937166.1 AA937166 ok13a08.s1 Soares_NSF_F8...	888	0.0
gi 10941529 gb BF111839.1 BF111839 7j36c03.x1 Soares_NSF_F8...	886	0.0
gi 5837771 gb AI990886.1 AI990886 ws24b02.x1 NCI_CGAP_GC6 H...	880	0.0
gi 3960152 gb AI300806.1 AI300806 qn47b02.x1 NCI_CGAP_Kid5 ...	880	0.0
gi 12041329 gb BF725418.1 BF725418 bx15f11.y1 Human Iris cD...	878	0.0
gi 10809455 gb BF055559.1 BF055559 7j81h04.x1 Soares_NSF_F8...	872	0.0
gi 5366102 gb AI800708.1 AI800708 tc13c01.x1 Soares_NhHMPu...	872	0.0
gi 10150139 gb BE736147.1 BE736147 601307226F1 NIH_MGC_39 H...	864	0.0
gi 14568272 gb BI117371.1 BI117371 602867919F1 NIH_MGC_7 Ho...	860	0.0
gi 2279509 gb AA535256.1 AA535256 nf93b07.s1 NCI_CGAP_Co3 H...	860	0.0

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gi|8908766|gb|BE221448.1|BE221448 hu25b07.x1 NCI_CGAP_Mel15... 858 0.0
 gi|10938643|gb|BF108953.1|BF108953 7l55a06.x1 Soares_NSF_F8... 856 0.0
 gi|6026228|gb|AW071230.1|AW071230 wz23e02.x1 Soares_Dieckgr... 841 0.0
 gi|11251209|gb|BF304472.1|BF304472 601887831F1 NIH_MGC_17 H... 811 0.0

>gi|14602730|gb|AAH09881.1|AAH09881 Unknown (protein for MGC:16483)
 [Homo sapiens]

EST Search:

Organ: placenta
 Tissue type: choriocarcinoma

Organ: lung
 Tissue type: small cell carcinoma

Organ: bone marrow
 Tissue type: from acute myelogenous leukemia

Organ: brain
 Tissue type: anaplastic oligodendrogloma

	Score	E	
Sequences producing significant alignments:		(bits)	Value
gi 13412286 gb BG480007.1 BG480007 602527580F1 NIH_MGC_21 H...	1469	0.0	
gi 14568272 gb BI117371.1 BI117371 602867919F1 NIH_MGC_7 Ho...	1467	0.0	
gi 10388276 gb BE900363.1 BE900363 601673230F1 NIH_MGC_21 H...	1409	0.0	
gi 10394942 gb BE903479.1 BE903479 601676737F1 NIH_MGC_21 H...	1364	0.0	
gi 10162791 gb BE748799.1 BE748799 601572007T1 NIH_MGC_55 H...	1312	0.0	
gi 5545428 gb AI871379.1 AI871379 wl81d08.x1 NCI_CGAP_Bm25...	1298	0.0	
gi 14169716 gb BG822129.1 BG822129 602726271F1 NIH_MGC_15 H...	1291	0.0	
gi 12670294 gb BG163591.1 BG163591 602338741F1 NIH_MGC_89 H...	1207	0.0	
gi 5178261 gb AI762594.1 AI762594 wi56b09.x1 NCI_CGAP_Co16 ...	1185	0.0	
gi 9140120 gb BE266541.1 BE266541 601193528F1 NIH_MGC_7 Hom...	1168	0.0	
gi 6709871 gb AW300271.1 AW300271 xs58h07.x1 NCI_CGAP_Kid11...	1144	0.0	
gi 9803527 gb BE559808.1 BE559808 601346972F1 NIH_MGC_8 Hom...	1132	0.0	
gi 10150139 gb BE736147.1 BE736147 601307226F1 NIH_MGC_39 H...	1094	0.0	
gi 12041329 gb BF725418.1 BF725418 bx15f11.y1 Human Iris cD...	1092	0.0	
gi 5108921 gb AI740633.1 AI740633 wg23g01.x1 Soares_NSF_F8...	1090	0.0	
gi 4372796 gb AI479628.1 AI479628 tm32d07.x1 NCI_CGAP_CLL1 ...	1067	0.0	
gi 6570140 gb AW237763.1 AW237763 xm81b04.x1 NCI_CGAP_Kid11...	1059	0.0	
gi 8169897 gb AW978626.1 AW978626 EST390735 MAGE resequence...	1047	0.0	
gi 5540213 gb AI867197.1 AI867197 wa01c10.x1 NCI_CGAP_Kid11...	1045	0.0	
gi 11448154 gb BF435839.1 BF435839 nab42e01.x1 Soares_NSF_F...	1035	0.0	
gi 10938383 gb BF108693.1 BF108693 7l44e02.x1 Soares_NSF_F8...	1033	0.0	
gi 10036058 gb BE675517.1 BE675517 7f10f02.x1 NCI_CGAP_CLL1...	1029	0.0	
gi 9970354 gb BE646054.1 BE646054 7e92d04.x1 NCI_CGAP_CLL1 ...	1011	0.0	
gi 5933828 gb AW058189.1 AW058189 wv83h01.x1 Soares_thymus...	1011	0.0	
gi 11251209 gb BF304472.1 BF304472 601887831F1 NIH_MGC_17 H...	1009	0.0	
gi 4190356 gb AI380503.1 AI380503 tf95d02.x1 NCI_CGAP_CLL1 ...	1007	0.0	
gi 5113008 gb AI744631.1 AI744631 wg04g09.x1 Soares_NSF_F8...	1005	0.0	
gi 5450901 gb AI830241.1 AI830241 wj78h11.x1 NCI_CGAP_Lu19 ...	1003	0.0	
gi 4598007 gb AI588959.1 AI588959 tk15d10.x1 Soares_NhHMPu...	999	0.0	
gi 4113265 gb AI361644.1 AI361644 qy86d07.x1 NCI_CGAP_Brn25...	987	0.0	
gi 11082796 gb BF195666.1 BF195666 7n86g02.x1 NCI_CGAP_Ov18...	977	0.0	

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gi|5232040|gb|AI765531.1|AI765531 wi81b11.x1 NCI_CGAP_Kid12... 973 0.0
 gi|2463985|gb|AA612947.1|AA612947 nq38e11.s1 NCI_CGAP_Co10 ... 963 0.0
 gi|12758392|gb|BG248576.1|BG248576 602400744F1 NIH_MGC_15 H... 957 0.0
 gi|11682572|gb|BF590248.1|BF590248 nab22a02.x1 Soares_NSF_F... 957 0.0
 gi|4311958|gb|AI457940.1|AI457940 tj55h09.x1 Soares_NSF_F8... 957 0.0
 gi|9122527|gb|BE252388.1|BE252388 601117771F1 NIH_MGC_16 Ho... 954 0.0
 gi|6710832|gb|AW301155.1|AW301155 xs57a11.x1 NCI_CGAP_Kid11... 950 0.0
 gi|5663387|gb|AI927423.1|AI927423 wo75e11.x1 NCI_CGAP_Pr22 ... 950 0.0
 gi|5766733|gb|AI969915.1|AI969915 wq77e03.x1 NCI_CGAP_Pr28 ... 948 0.0
 gi|5664220|gb|AI928256.1|AI928256 wo67a08.x1 NCI_CGAP_Pr22 ... 946 0.0
 gi|1377082|gb|W68057.1|W68057 zd42h12.r1 Soares_fetal_heart... 938 0.0
 gi|6746198|gb|AW316942.1|AW316942 xw13a08.x1 NCI_CGAP_Brn53... 934 0.0
 gi|1959057|gb|AA306658.1|AA306658 EST177664 Jurkat T-cells ... 934 0.0
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 gi|12358324|gb|BF941004.1|BF941004 hu63a05.x1 NCI_CGAP_Brn4... 908 0.0
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 gi|14057456|gb|BG746803.1|BG746803 602704139F1 NIH_MGC_15 H... 904 0.0
 gi|10819930|gb|BF061020.1|BF061020 7j62f12.x1 Soares_NSF_F8... 898 0.0
 gi|5837771|gb|AI990886.1|AI990886 ws24b02.x1 NCI_CGAP_GC6 H... 896 0.0
 gi|10941529|gb|BF111839.1|BF111839 7l36c03.x1 Soares_NSF_F8... 894 0.0
 gi|10809455|gb|BF055559.1|BF055559 7j81h04.x1 Soares_NSF_F8... 888 0.0
 gi|5366102|gb|AI800708.1|AI800708 tc13c01.x1 Soares_NhHMPu... 888 0.0
 gi|6836760|gb|AW340134.1|AW340134 hc93g05.x1 SoaresNFL_T_G... 882 0.0
 gi|3960152|gb|AI300806.1|AI300806 qr47b02.x1 NCI_CGAP_Kid5 ... 880 0.0
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 gi|8908766|gb|BE221448.1|BE221448 hu25b07.x1 NCI_CGAP_Mel15... 874 0.0
 gi|10938643|gb|BF108953.1|BF108953 7l55a06.x1 Soares_NSF_F8... 872 0.0
 gi|2740699|gb|AA722992.1|AA722992 zg89c05.s1 Soares_fetal_h... 872 0.0
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 gi|2675026|gb|AA688120.1|AA688120 nv15h04.s1 NCI_CGAP_Pr22 ... 864 0.0
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 gi|6026228|gb|AW071230.1|AW071230 wz23e02.x1 Soares_Dieckgr... 854 0.0
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 gi|1670790|gb|AA115759.1|AA115759 zk96g06.s1 Soares_pregnant... 842 0.0
 gi|14620762|gb|BI160761.1|BI160761 602864839F1 NIH_MGC_42 H... 831 0.0
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 gi|3751123|gb|AI198517.1|AI198517 qf94h01.x1 Soares_placent... 815 0.0
 gi|3739896|gb|AI188687.1|AI188687 qd10g06.x1 Soares_placent... 795 0.0
 gi|11683021|gb|BF590610.1|BF590610 7h40f10.x1 NCI_CGAP_Co16... 791 0.0
 gi|5449740|gb|AI829069.1|AI829069 wj38c05.x1 NCI_CGAP_Lu19 ... 791 0.0
 gi|2336957|gb|AA565318.1|AA565318 nj37c11.s1 NCI_CGAP_AA1 H... 791 0.0
 gi|1690504|gb|AA133534.1|AA133534 zk96g06.r1 Soares_pregnant... 787 0.0
 gi|3232294|gb|AI017958.1|AI017958 ou30b01.x1 SoaresNFL_T_G... 777 0.0
 gi|4223386|gb|AI393839.1|AI393839 tg59d07.x1 Soares_NSF_F8... 763 0.0
 gi|5176495|gb|AI760828.1|AI760828 wh96e10.x1 NCI_CGAP CLL1 ... 755 0.0
 gi|4113115|gb|AI361494.1|AI361494 qy48c02.x1 NCI_CGAP_Brn23... 739 0.0
 gi|3117502|gb|AA953355.1|AA953355 oo88c12.s1 NCI_CGAP_Kid5 ... 739 0.0
 gi|1544002|gb|AA053347.1|AA053347 zl70h05.s1 Stratagene col... 737 0.0
 gi|2241423|gb|AA505286.1|AA505286 nh95c04.s1 NCI_CGAP_Br2 H... 728 0.0
 gi|2218486|gb|AA488884.1|AA488884 aa55f09.s1 NCI_CGAP_GCB1 ... 728 0.0
 gi|880732|gb|H15912.1|H15912 yl27c07.s1 Soares breast 3NbHB... 726 0.0

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gi|2445628|gb|AA604764.1|AA604764 no84f06.s1 NCI_CGAP_AA1 H... 724 0.0
gi|3741170|gb|AI189961.1|AI189961 qd19f09.x1 Soares_placent... 722 0.0
gi|8143250|gb|AW953567.1|AW953567 EST365637 MAGE resequence... 720 0.0
gi|6142870|gb|AW138552.1|AW138552 UI-H-BI1-abx-f-03-0-UI.s1... 712 0.0
gi|2901576|gb|AA828477.1|AA828477 oc42g04.s1 NCI_CGAP_GCB1 ... 694 0.0
gi|651330|gb|T49470.1|T49470 ya75g04.s1 Stratagene placenta... 692 0.0
gi|5544123|gb|AI870155.1|AI870155 wk99b03.x1 NCI_CGAP_Lu19 ... 688 0.0
gi|843074|gb|R69557.1|R69557 yj82h11.r1 Soares breast 2NbHB... 684 0.0
gi|12397550|gb|BF991225.1|BF991225 CM0-GN0162-271000-627-h0... 676 0.0
gi|856105|gb|R79824.1|R79824 yi89a05.s1 Soares placenta Nb2... 676 0.0
gi|7039183|gb|AW469077.1|AW469077 hc76d11.x1 NCI_CGAP_Gas4 ... 664 0.0
gi|12356691|gb|BF939371.1|BF939371 nad94e01.x1 NCI_CGAP_Ov1... 658 0.0
```

>gi|14602625|gb|AAH09830.1|AAH09830 PAN2 protein [Homo sapiens]

EST Search:

Tissue type: placenta

Tissue type: T cells from T cell leukemia

Tissue type: Adult brain

Organ: brain

Tissue type: hippocampus

Tissue type: primary B-cells from tonsils (cell line)

Organ: colon

Tissue type: adenocarcinoma

Sequences producing significant alignments:

(bits) Value

gi 12875608 emb AL543130.1 AL543130 AL543130 LTI_NFL006_PL2...	1832	0.0
gi 12943976 emb AL579184.1 AL579184 AL579184 LTI_FL012_TC1 ...	1727	0.0
gi 12915979 emb AL565020.1 AL565020 AL565020 LTI_FL015_Bm1...	1505	0.0
gi 12887406 emb AL550433.1 AL550433 AL550433 LTI_NFL006_PL2...	1455	0.0
gi 13974137 gb BG702619.1 BG702619 602684333F1 NIH_MGC_95 H...	1429	0.0
gi 14069852 gb BG759199.1 BG759199 602710860F1 NIH_MGC_48 H...	1423	0.0
gi 10319309 gb BE870533.1 BE870533 601448228F1 NIH_MGC_65 H...	1283	0.0
gi 10746413 gb BF037954.1 BF037954 601461651F1 NIH_MGC_66 H...	1275	0.0
gi 12943974 emb AL579183.1 AL579183 AL579183 LTI_FL012_TC1 ...	1263	0.0
gi 10290446 dbj AV688583.1 AV688583 AV688583 GKC Homo sapie...	1245	0.0
gi 10967752 gb BF128712.1 BF128712 601810983F1 NIH_MGC_48 H...	1235	0.0
gi 10203453 gb BE782255.1 BE782255 601466690F1 NIH_MGC_67 H...	1231	0.0
gi 14050138 gb BG779821.1 BG779821 602667289F1 NIH_MGC_60 H...	1205	0.0
gi 10919908 dbj AV762060.1 AV762060 AV762060 MDS Homo sapie...	1183	0.0
gi 12934358 emb AL574292.1 AL574292 AL574292 LTI_NFL006_PL2...	1104	0.0
gi 10289308 dbj AV687445.1 AV687445 AV687445 GKC Homo sapie...	1100	0.0
gi 12875574 emb AL543096.1 AL543096 AL543096 LTI_NFL006_PL2...	1080	0.0
gi 13339671 gb BG433165.1 BG433165 602496421F1 NIH_MGC_75 H...	1076	0.0
gi 10967874 gb BF128834.1 BF128834 601811019F1 NIH_MGC_48 H...	1059	0.0
gi 10294954 dbj AV693091.1 AV693091 AV693091 GKC Homo sapie...	1039	0.0
gi 10969105 gb BF130065.1 BF130065 601817940F1 NIH_MGC_58 H...	1007	0.0
gi 10736896 gb BF029184.1 BF029184 601764696F1 NIH_MGC_53 H...	922	0.0

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gi|12615542|gb|BG122033.1|BG122033 602349409F1 NIH_MGC_90 H... 852 0.0
 gi|4004205|gb|AI309334.1|AI309334 qo80d08.x1 NCI_CGAP_Kid5 ... 821 0.0
 gi|1281106|gb|W07093.1|W07093 za93c06.r1 Soares_fetal_lung... 811 0.0
 gi|10300054|dbj|AV698167.1|AV698167 AV698167 GKC Homo sapie... 793 0.0
 gi|1376483|gb|W67612.1|W67612 zd41c08.r1 Soares_fetal_heart... 787 0.0
 gi|6876390|gb|AW371736.1|AW371736 CM0-BT0304-111199-093-d11... 785 0.0
 gi|13576852|gb|BG569199.1|BG569199 602588473F1 NIH_MGC_76 H... 769 0.0
 gi|1898399|gb|AA262838.1|AA262838 zs24c11.r1 NCI_CGAP_GCB1 ... 763 0.0
 gi|8155033|gb|AW965197.1|AW965197 EST377270 MAGE resequence... 753 0.0
 gi|8155021|gb|AW965185.1|AW965185 EST377258 MAGE resequence... 753 0.0
 gi|10295847|dbj|AV693984.1|AV693984 AV693984 GKC Homo sapie... 720 0.0
 gi|10208100|gb|BE786902.1|BE786902 601477765F1 NIH_MGC_68 H... 720 0.0
 gi|10294947|dbj|AV693084.1|AV693084 AV693084 GKC Homo sapie... 708 0.0
 gi|13791909|gb|BG654500.1|BG654500 ib41c07.y1 HR85 islet Ho... 680 0.0
 gi|12915977|emb|AL565019.1|AL565019 AL565019 LTI_FL015_Bm1... 678 0.0
 gi|10297856|dbj|AV695993.1|AV695993 AV695993 GKC Homo sapie... 652 0.0
 gi|1997881|gb|AA345644.1|AA345644 EST51687 Gall bladder II ... 589 e-166
 gi|4439638|gb|AI525503.1|AI525503 PT1.4_B01.r tumor1 Homo... 567 e-159
 gi|13703589|gb|BG181902.1|BG181902 RST760 Athersys RAGE Lib... 541 e-151
 gi|8907221|gb|BE219903.1|BE219903 hv64c09.x1 NCI_CGAP_Lu24 ... 531 e-148
 gi|841904|gb|R68387.1|R68387 yh99g01.r1 Soares placenta Nb2... 529 e-148
 gi|13545980|gb|BG547315.1|BG547315 602574734F1 NIH_MGC_77 H... 359 1e-96
 gi|1239209|gb|N76631.1|N76631 yz79h10.r1 Soares_multiple_sc... 323 7e-86
 gi|13319146|gb|BG413593.1|BG413593 7j63f11.x1 Soares_NSF_F8... 313 7e-83
 gi|5811063|gb|AI983844.1|AI983844 wt51d12.x1 NCI_CGAP_Pan1 ... 305 2e-80
 gi|5850543|gb|AW003627.1|AW003627 wx34e03.x1 NCI_CGAP_Pit1 ... 303 7e-80
 gi|13791976|gb|BG654567.1|BG654567 ib41c07.x1 HR85 islet Ho... 291 3e-76
 gi|1844851|gb|AA224309.1|AA224309 zr15f05.r1 Stratagene NT2... 274 6e-71
 gi|5635411|gb|AI915556.1|AI915556 wg30e08.x1 Soares_NSF_F8... 260 9e-67
 gi|2366350|dbj|C75288.1|C75288 C75288 Human pancreatic isle... 258 4e-66
 gi|4534171|gb|AI570797.1|AI570797 tr67c10.x1 NCI_CGAP_Pan1 ... 250 9e-64
 gi|12242488|gb|BF854705.1|BF854705 RC6-FN0202-271000-011-C0... 238 3e-60
 gi|2437676|gb|AA603815.1|AA603815 nn87e11.s1 NCI_CGAP_Br2 H... 216 1e-53
 gi|4989930|gb|AI702030.1|AI702030 tq20e05.x1 NCI_CGAP_Ut1 H... 196 1e-47
 gi|11159725|gb|BF245883.1|BF245883 601864059F1 NIH_MGC_57 H... 180 7e-43
 gi|12245429|gb|BF857685.1|BF857685 RC5-FT0194-061100-031-A0... 170 7e-40
 gi|12243397|gb|BF855653.1|BF855653 RC6-FN0202-171100-012-D0... 170 7e-40
 gi|11019045|dbj|AU157524.1|AU157524 AU157524 PLACE1 Homo sa... 168 3e-39
 gi|3424383|gb|AI085960.1|AI085960 oz86g08.x1 Soares_senesce... 167 1e-38
 gi|12242489|gb|BF854706.1|BF854706 RC6-FN0202-271000-011-C0... 163 2e-37
 gi|5177517|gb|AI761761.1|AI761761 wg68a02.x1 Soares_NSF_F8... 157 1e-35
 gi|3075842|gb|AA926945.1|AA926945 om68g02.s1 NCI_CGAP_GC4 H... 139 2e-30
 gi|1225675|gb|N69514.1|N69514 yz79h10.s1 Soares_multiple_sc... 119 2e-24
 gi|6464995|gb|AW190515.1|AW190515 xl63b10.x1 NCI_CGAP_Pan1 ... 113 1e-22
 gi|3736368|gb|AI185730.1|AI185730 qe33b10.s1 Soares_fetal_l... 111 5e-22
 gi|6199686|gb|AW151788.1|AW151788 xf69c11.x1 NCI_CGAP_Gas4 ... 109 2e-21
 gi|4533666|gb|AI570292.1|AI570292 to77d10.x1 NCI_CGAP_Gas4 ... 109 2e-21
 gi|4648078|gb|AI623153.1|AI623153 tu89d03.x1 NCI_CGAP_Gas4 ... 105 3e-20
 gi|5744801|gb|AI952491.1|AI952491 wx74e04.x1 NCI_CGAP_Ov38 ... 92 5e-16
 gi|3870043|gb|AI261840.1|AI261840 qk11a10.x1 NCI_CGAP_Kid3 ... 90 2e-15
 gi|6834091|gb|AW337465.1|AW337465 xx57d09.x1 NCI_CGAP_Lym12... 82 5e-13
 gi|1432534|dbj|C00304.1|C00304 HUMGS0006005 Human adult (K.... 72 4e-10
 gi|12767084|gb|BG257268.1|BG257268 602377984F1 NIH_MGC_92 H... 44 0.10
 gi|1367064|gb|W60305.1|W60305 zd29e01.s1 Soares_fetal_heart... 44 0.10
 gi|14065766|gb|BG755113.1|BG755113 602711428F1 NIH_MGC_48 H... 40 1.6
 gi|8472627|gb|BE082325.1|BE082325 QV2-BT0636-070500-194-h05... 40 1.6
 gi|14502208|gb|BI083878.1|BI083878 602869109F1 NIH_MGC_102 ... 38 6.2

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gi|14391900|gb|BG987830.1|BG987830 CM3-HT1150-110101-623-h0... 38 6.2
gi|14072079|gb|BG761426.1|BG761426 602718627F1 NIH_MGC_49 H... 38 6.2
gi|13411218|gb|BG478939.1|BG478939 602525701F1 NIH_MGC_21 H... 38 6.2
gi|12916582|emb|AL565322.1|AL565322 AL565322 LTI_FL013_FBrn... 38 6.2
gi|12288761|gb|BF897302.1|BF897302 IL2-MT0179-281100-255-C0... 38 6.2
gi|12057953|gb|BF732878.1|BF732878 nae16g05.x1 NCI_CGAP_Ov1... 38 6.2
gi|11297817|gb|BF327069.1|BF327069 RC1-BN0056-230200-012-e0... 38 6.2
gi|11766564|gb|BE963146.2|BE963146 601656952R1 NIH_MGC_67 H... 38 6.2
gi|11102818|gb|BF209128.1|BF209128 601872828F1 NIH_MGC_54 H... 38 6.2
gi|10357166|gb|BE894606.1|BE894606 601433223F1 NIH_MGC_72 H... 38 6.2
gi|10314262|gb|BE865486.1|BE865486 601677815F1 NIH_MGC_53 H... 38 6.2
gi|10201679|gb|BE780481.1|BE780481 601468751F1 NIH_MGC_67 H... 38 6.2
gi|10162316|gb|BE748324.1|BE748324 601572007F1 NIH_MGC_55 H... 38 6.2
gi|8485301|gb|BE094848.1|BE094848 CM2-BT0790-180400-164-a12... 38 6.2
gi|7280198|gb|AW593003.1|AW593003 hg07b03.x1 Soares_NFL_T_G... 38 6.2
gi|6705383|gb|AW298747.1|AW298747 UI-H-BW0-ajq-b-01-0-UI.s1... 38 6.2
gi|6462898|gb|AW188462.1|AW188462 xj99b07.x1 NCI_CGAP_Co18 ... 38 6.2
gi|6037073|gb|AW081921.1|AW081921 xb57d02.x1 NCI_CGAP_Eso2 ... 38 6.2
gi|5664247|gb|AI928283.1|AI928283 wo67d07.x1 NCI_CGAP_Pr22 ... 38 6.2
gi|3890823|gb|AI271656.1|AI271656 qi30h05.x1 Soares_NhHMPu... 38 6.2
gi|750752|gb|R01016.1|R01016 ye87a12.r1 Soares fetal liver ... 38 6.2

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>gi|14724826|ref|XP_043555.1| hypothetical protein FLJ14431 [Homo sapiens]

EST Search:

Tissue type: Adrenal gland

Organ: Liver and Spleen

Develop. stage: 20 week-post conception fetus

Organ: liver

Tissue type: adenocarcinoma, cell line

Organ: lung

Tissue type: carcinoid

Sequences producing significant alignments:

(bits) Value

```

gi|8165991|gb|AW974788.1|AW974788 EST386893 MAGE resequence... 1057 0.0
gi|10721718|gb|AV704400.1|AV704400 AV704400 ADB Homo sapie... 1035 0.0
gi|1424282|gb|W91890.1|W91890 zh47a06.r1 Soares_fetal_liver... 1031 0.0
gi|12613045|gb|BG119539.1|BG119539 602347238F1 NIH_MGC_90 H... 989 0.0
gi|10940429|gb|BF110739.1|BF110739 7n56b09.x1 NCI_CGAP_Lu24... 971 0.0
gi|2657822|gb|AA677300.1|AA677300 zj61f10.s1 Soares_fetal_l... 900 0.0
gi|2584140|gb|AA652488.1|AA652488 ns70b08.s1 NCI_CGAP_Pr2 H... 890 0.0
gi|1472212|gb|AA011185.1|AA011185 ze22d01.s1 Soares_fetal_h... 793 0.0
gi|14320377|gb|BG925854.1|BG925854 HNC21-1-B1.R HNC (Human ... 773 0.0
gi|1388213|gb|W78181.1|W78181 zd68a06.r1 Soares_fetal_heart... 763 0.0
gi|1406088|gb|W90098.1|W90098 zh77e04.s1 Soares_fetal_liver... 714 0.0
gi|2657062|gb|AA676540.1|AA676540 zi38c04.s1 Soares_fetal_l... 698 0.0
gi|14166353|gb|BG818766.1|BG818766 602779096F2 NCI_CGAP_Brn... 642 0.0
gi|1406186|gb|W90196.1|W90196 zh77e04.r1 Soares_fetal_liver... 636 e-180

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>gi|14782791|ref|XP_042583.1| FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like [Homo sapiens]

EST Search:

Tissues: Organ: lung
 Tissue type: small cell carcinoma
 Cell line: MGC3

Organ: pancreas
 Tissue type: adenocarcinoma

Tissue type: placenta

Organ: placenta
 Tissue type: choriocarcinoma

Tissue type: cervical carcinoma cell line

Organ: pancreas
 Tissue type: epithelioid carcinoma cell line

Sequences producing significant alignments: (bits) Value

gi 10214178 gb BE792980.1 BE792980	601585653F1 NIH_MGC_7 Ho...	1384	0.0
gi 10149821 gb BE735829.1 BE735829	601305146F1 NIH_MGC_39 H...	1352	0.0
gi 12897211 emb AL555459.1 AL555459	AL555459 LTI_NFL006 PL2...	1344	0.0
gi 10391209 gb BE901734.1 BE901734	601675345F1 NIH_MGC_21 H...	1285	0.0
gi 14805093 gb BI253554.1 BI253554	602973478F1 NIH_MGC_12 H...	1251	0.0
gi 14619885 gb BI159884.1 BI159884	602863711F1 NIH_MGC_42 H...	1245	0.0
gi 2703586 gb AA700623.1 AA700623	zi43a04.s1 Soares_fetal...	1203	0.0
gi 12897209 emb AL555458.1 AL555458	AL555458 LTI_NFL006 PL2...	1183	0.0
gi 11613994 gb BF526631.1 BF526631	602070755F1 NCI_CGAP_Brn...	1181	0.0
gi 5394035 gb AI807469.1 AI807469	wf48b08.x1 Soares_NFL_T_G...	1170	0.0
gi 12345465 gb BF978250.1 BF978250	602148205F1 NIH_MGC_62 H...	1142	0.0
gi 5878587 gb AW025057.1 AW025057	wu93f03.x1 NCI_CGAP_Kid3 ...	1120	0.0
gi 5839154 gb AI992249.1 AI992249	ws41d10.x1 NCI_CGAP_Brn25...	1067	0.0
gi 12411526 gb BG025183.1 BG025183	602276160F1 NIH_MGC_85 H...	1027	0.0
gi 3766024 gb AI207352.1 AI207352	qq26d10.x1 NCI_CGAP_Kid3 ...	1027	0.0
gi 4268048 gb AI422117.1 AI422117	tf40g03.x1 NCI_CGAP_Brn23...	989	0.0
gi 2568438 gb AA643220.1 AA643220	nr96h03.s1 NCI_CGAP_Pr25 ...	983	0.0
gi 4110767 gb AI359146.1 AI359146	qy26b08.x1 NCI_CGAP_Brn23...	906	0.0
gi 5838543 gb AI991715.1 AI991715	wf48a04.x1 NCI_CGAP_Pan1 ...	850	0.0
gi 5397037 gb AI810471.1 AI810471	wb89a09.x1 NCI_CGAP_Pr28 ...	801	0.0
gi 2942259 gb AA854721.1 AA854721	aj76h02.s1 Soares_parathy...	797	0.0
gi 4190811 gb AI380946.1 AI380946	tg18c12.x1 NCI_CGAP CLL1 ...	779	0.0
gi 3425472 gb AI087049.1 AI087049	oy70b11.x1 NCI_CGAP CLL1 ...	761	0.0
gi 6039316 gb AW084164.1 AW084164	xc48b09.x1 NCI_CGAP_Eso2 ...	755	0.0
gi 3202509 gb AI002175.1 AI002175	oq85b06.s1 NCI_CGAP_Kid6 ...	747	0.0
gi 2785843 gb AA745857.1 AA745857	ny93f03.s1 NCI_CGAP_GCB1 ...	745	0.0
gi 1422483 gb W93361.1 W93361	zd94g06.s1 Soares_fetal_heart...	731	0.0

>gi|14754051|ref|XP_003611.3| similar to oxidoreductase UCPA (H. sapiens) [Homo sapiens]

EST Search:

Organ: brain
 Tissue type: neuroblastoma cells

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Tissue type: placenta

Organ: kidney

Organ: lung

Tissue type: large cell carcinoma

Organ: brain

Tissue type: hypothalamus

Organ: parathyroid gland

Tissue type: parathyroid tumor

Sequences producing significant alignments: (bits) Value

gi 12786589 emb AL523096.1 AL523096 AL523096 LTI_NFL003_NBC...	1550	0.0
gi 12889983 emb AL551741.1 AL551741 AL551741 LTI_NFL006_PL2...	1457	0.0
gi 12936195 emb AL575230.1 AL575230 AL575230 LTI_NFL006_PL2...	1296	0.0
gi 12793625 emb AL530132.1 AL530132 AL530132.LTI_NFL001_NBC...	1289	0.0
gi 13294054 gb BG400606.1 BG400606 602464263F1 NIH_MGC_75 H...	1271	0.0
gi 13452667 gb BG491155.1 BG491155 602518792F1 NIH_MGC_18 H...	1237	0.0
gi 13982652 gb BG706873.1 BG706873 602672037F1 NIH_MGC_96 H...	1229	0.0
gi 3281013 gb AI041819.1 AI041819 oy34a10.x1 Soares_parathy...	1191	0.0
gi 13976480 gb BG703780.1 BG703780 602686804F1 NIH_MGC_95 H...	1176	0.0
gi 14051133 gb BG740480.1 BG740480 602633875F1 NCI_CGAP_Skn...	1170	0.0
gi 13545674 gb BG547009.1 BG547009 602573805F1 NIH_MGC_77 H...	1168	0.0
gi 12793624 emb AL530131.1 AL530131 AL530131 LTI_NFL001_NBC...	1168	0.0
gi 13039621 gb BG286600.1 BG286600 602381608F1 NIH_MGC_93 H...	1152	0.0
gi 11257955 gb BF310393.1 BF310393 601895043F1 NIH_MGC_19 H...	1146	0.0
gi 2839375 gb AA780044.1 AA780044 zj24e12.s1 Soares_fetal_I...	1142	0.0
gi 8154981 gb AW965145.1 AW965145 EST377218 MAGE resequence...	1138	0.0
gi 11265005 gb BF316648.1 BF316648 601903206F1 NIH_MGC_19 H...	1134	0.0
gi 3238050 gb AI022809.1 AI022809 ow55f02.x1 Soares_parathy...	1104	0.0
gi 4073201 gb AI336274.1 AI336274 q45e02.x1 Soares_fetal_I...	1096	0.0
gi 13544541 gb BG545876.1 BG545876 602573161F1 NIH_MGC_77 H...	1094	0.0
gi 12598260 gb BG104418.1 BG104418 602311036F1 NIH_MGC_20 H...	1086	0.0
gi 12598014 gb BG104172.1 BG104172 602310736F1 NIH_MGC_20 H...	1080	0.0
gi 12606210 gb BG112704.1 BG112704 602282264F1 NIH_MGC_86 H...	1065	0.0
gi 2877836 gb AA808430.1 AA808430 oe53b08.s1 NCI_CGAP_Lu5 H...	1057	0.0
gi 6471396 gb AW192697.1 AW192697 xl48h04.x1 NCI_CGAP_Pan1 ...	1037	0.0
gi 9323894 gb BE378429.1 BE378429 601236767F1 NIH_MGC_44 Ho...	1035	0.0
gi 5109073 gb AI740785.1 AI740785 wg24b10.x1 Soares_NSF_F8...	997	0.0
gi 5813571 gb AI986294.1 AI986294 wz64c08.x1 NCI_CGAP_Mel15...	987	0.0
gi 3400111 gb AI073467.1 AI073467 ov45a08.x1 Soares_testis...	983	0.0
gi 6228615 gb AW157214.1 AW157214 au92h07.x1 Schneider feta...	981	0.0
gi 12910323 emb AL562168.1 AL562168 AL562168 LTI_NFL003_NBC...	979	0.0
gi 9186202 gb BE302454.1 BE302454 ba65f04.y1 NIH_MGC_20 Hom...	979	0.0
gi 9186195 gb BE302447.1 BE302447 ba65e04.y1 NIH_MGC_20 Hom...	963	0.0
gi 12875811 emb AL543333.1 AL543333 AL543333 LTI_NFL006_PL2...	957	0.0
gi 2993433 gb AA883903.1 AA883903 aj13a01.s1 Soares_parathy...	946	0.0
gi 4435368 gb AI521233.1 AI521233 to66f02.x1 NCI_CGAP_Gas4 ...	940	0.0
gi 10350081 gb BE891095.1 BE891095 601432208F1 NIH_MGC_72 H...	922	0.0
gi 8750771 gb BE207373.1 BE207373 ba65e04.x1 NIH_MGC_20 Hom...	920	0.0
gi 5858190 gb AW009412.1 AW009412 ws82c11.x1 NCI_CGAP_Co3 H...	920	0.0
gi 3255193 gb AI034240.1 AI034240 ow09h12.x1 Soares_parathy...	916	0.0
gi 2324986 gb AA554447.1 AA554447 nl14h10.s1 NCI_CGAP_Br2 H...	916	0.0
gi 5546002 gb AI871953.1 AI871953 wm53h05.x1 NCI_CGAP_Ut2 H...	914	0.0

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gi|2955773|gb|AA863294.1|AA863294 og93b12.s1 NCI_CGAP_Kid5 ... 904 0.0
gi|4598887|gb|AI589839.1|AI589839 tm81a02.x1 NCI_CGAP_Brn25... 900 0.0

>gi|13278690|gb|AAH04126.1|AAH04126 (BC004126) DKFZP566O084 protein

EST search:

99% identities to ESTs found in small cell lung cancer (tissue, cell line), ovary adenocarcinoma (cell line); pancreas adenocarcinoma (tissue); kidney hypernephroma (cell line); skin/melanotic melanoma

Sequences producing significant alignments: (bits) Value

gi 10219393 gb BE798195.1 BE798195 601582662F1 NIH_MGC_7 Ho...	1441	0.0
gi 10156033 gb BE742041.1 BE742041 601594721F1 NIH_MGC_9 Ho...	1423	0.0
gi 10150854 gb BE736951.1 BE736951 601306912F1 NIH_MGC_39 H...	1415	0.0
gi 10216541 gb BE795343.1 BE795343 601586662F1 NIH_MGC_7 Ho...	1392	0.0
gi 12678574 gb BG171871.1 BG171871 602322675F1 NIH_MGC_89 H...	1287	0.0
gi 9331772 gb BE386407.1 BE386407 601273578F1 NIH_MGC_20 Ho...	1265	0.0
gi 9148949 gb BE274012.1 BE274012 601104628F1 NIH_MGC_14 Ho...	1255	0.0
gi 9334357 gb BE388992.1 BE388992 601284814F1 NIH_MGC_44 Ho...	1237	0.0
gi 5674161 gb AI935291.1 AI935291 wp16e06.x1 NCI_CGAP_Lu19 ...	1209	0.0
gi 13409767 gb BG477488.1 BG477488 602521540F1 NIH_MGC_20 H...	1180	0.0
gi 9335068 gb BE389703.1 BE389703 601281945F1 NIH_MGC_44 Ho...	1180	0.0
gi 10206923 gb BE785725.1 BE785725 601475291F1 NIH_MGC_68 H...	1160	0.0
gi 5920966 gb AW055263.1 AW055263 wz16b09.x1 NCI_CGAP_Ut4 H...	1148	0.0
gi 14073190 gb BG762537.1 BG762537 602733994F1 NIH_MGC_49 H...	1122	0.0
gi 4524063 gb AI565606.1 AI565606 to16g08.x1 NCI_CGAP_Ut2 H...	1090	0.0
gi 9335871 gb BE390506.1 BE390506 601284123F1 NIH_MGC_44 Ho...	1072	0.0
gi 1696026 gb AA134925.1 AA134925 zo23c07.s1 Stratagene col...	1023	0.0
gi 2900361 gb AA827998.1 AA827998 of10c11.s1 NCI_CGAP_Co12 ...	1021	0.0
gi 1383218 gb W73084.1 W73084 zd54a11.r1 Soares_fetal_heart...	1013	0.0
gi 1319356 gb W37623.1 W37623 zc12d10.r1 Soares_parathyroid...	963	0.0
gi 6026819 gb AW071733.1 AW071733 ws54h10.x1 NCI_CGAP_Brn25...	959	0.0
gi 4176147 gb AI376157.1 AI376157 ta59e06.x1 Soares_total_f...	940	0.0
gi 844959 gb R71442.1 R71442 yi51f01.r1 Soares_placenta_Nb2...	940	0.0
gi 6039788 gb AW084636.1 AW084636 xa45f07.x1 NCI_CGAP_Sar4 ...	924	0.0
gi 2809799 gb AA760869.1 AA760869 nz14h12.s1 NCI_CGAP_GCB1 ...	912	0.0
gi 6039287 gb AW084135.1 AW084135 xc37f09.x1 NCI_CGAP_Co20 ...	910	0.0
gi 1319357 gb W37624.1 W37624 zc12d10.s1 Soares_parathyroid...	910	0.0
gi 2525832 gb AA621956.1 AA621956 nq24a06.s1 NCI_CGAP_Co10 ...	902	0.0

>gi|14424501|gb|AAH09269.1|AAH09269 Unknown (protein for IMAGE:3140944) [Homo sapiens]

EST search:

97-99% identities to unknown cDNAs from lung carcinoid, neuroblastoma and mainly placenta

Sequences producing significant alignments: (bits) Value

gi 12790502 emb AL527009.1 AL527009 AL527009 LTI_NFL003_NBC...	1893	0.0
gi 12790549 emb AL527056.1 AL527056 AL527056 LTI_NFL003_NBC...	1709	0.0

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gi|12937462|emb|AL575872.1|AL575872 AL575872 LTI_NFL006_PL2... 1639 0.0
gi|12891750|emb|AL552647.1|AL552647 AL552647 LTI_NFL006_PL2... 1485 0.0
gi|12882168|emb|AL547782.1|AL547782 AL547782 LTI_NFL006_PL2... 1441 0.0
gi|8907775|gb|BE220457.1|BE220457 hv39e05.x1 NCI_CGAP_Lu24 ... 1251 0.0
gi|11448101|gb|BF435786.1|BF435786 nab41g04.x1 Soares_NSF_F... 1229 0.0
gi|10322956|gb|BE874180.1|BE874180 601484366F1 NIH_MGC_69 H... 1213 0.0
gi|13326948|gb|BG420442.1|BG420442 602452476F1 NIH_MGC_14 H... 1195 0.0
gi|10321982|gb|BE873206.1|BE873206 601451732F1 NIH_MGC_65 H... 1170 0.0
gi|11511078|gb|BF445940.1|BF445940 7p16f08.x1 NCI_CGAP_Br22... 1164 0.0
gi|10939112|gb|BF109422.1|BF109422 7l62g12.x1 Soares_NSF_F8... 1158 0.0
gi|5127852|gb|AI749588.1|AI749588 at30h03.x1 Barstead colon... 1148 0.0
gi|9146194|gb|BE271998.1|BE271998 601141171F1 NIH_MGC_9 Hom... 1122 0.0
gi|10821551|gb|BF062641.1|BF062641 7h63b10.x1 NCI_CGAP_Co16... 1067 0.0
gi|10030710|gb|BE670169.1|BE670169 7e31b01.x1 NCI_CGAP_Lu24... 1039 0.0
gi|12882218|emb|AL547808.1|AL547808 AL547808 LTI_NFL006_PL2... 1023 0.0
gi|5232056|gb|AI765547.1|AI765547 wi81d04.x1 NCI_CGAP_Kid12... 987 0.0
gi|3539100|gb|AI123334.1|AI123334 qa48b12.x1 Soares_NhHMPu... 987 0.0
gi|9706839|gb|BE504431.1|BE504431 hz86d06.x1 NCI_CGAP_Lu24 ... 975 0.0
gi|8278043|gb|BE017981.1|BE017981 bb74b11.y1 NIH_MGC_12 Hom... 973 0.0
gi|10813021|gb|BF059125.1|BF059125 7k66c05.x1 NCI_CGAP_GC6 ... 928 0.0
gi|8155988|gb|AW966152.1|AW966152 EST378225 MAGE resequence... 924 0.0
gi|9185243|gb|BE301495.1|BE301495 bb74b11.x1 NIH_MGC_12 Hom... 914 0.0
gi|5235374|gb|AI768865.1|AI768865 wj12g12.x1 NCI_CGAP_Kid12... 912 0.0
gi|12387026|gb|BF984214.1|BF984214 602307642F1 NIH_MGC_88 H... 906 0.0
gi|9512266|gb|BE466404.1|BE466404 hz21c10.x1 NCI_CGAP_GC6 H... 900 0.0

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>gi|13543367|gb|AAH05844.1|AAH05844 Unknown (protein for MGC:2723)
[Homo sapiens]

EST search: fetal and adult brain; neuroblastoma; leiomyosarcoma; pancreas carcinoma (cellline); Burkitt B cell lymphoma

Sequences producing significant alignments: (bits) Value

```

gi|12783362|emb|AL519869.1|AL519869 AL519869 LTI_NFL004_NBC... 1776 0.0
gi|12783361|emb|AL519868.1|AL519868 AL519868 LTI_NFL004_NBC... 1758 0.0
gi|12797239|emb|AL533746.1|AL533746 AL533746 LTI_FL013_FBrn... 1739 0.0
gi|12916262|emb|AL565162.1|AL565162 AL565162 LTI_FL015_Brn1... 1542 0.0
gi|12797054|emb|AL533561.1|AL533561 AL533561 LTI_FL015_Brn1... 1443 0.0
gi|11971146|gb|BF685738.1|BF685738 602140418F1 NIH_MGC_46 H... 1338 0.0
gi|14178399|gb|BG830812.1|BG830812 602767532F1 NIH_MGC_42 H... 1304 0.0
gi|12951379|emb|AL582918.1|AL582918 AL582918 LTI_NFL010_BC2... 1269 0.0
gi|10201129|gb|BE779931.1|BE779931 601467958F1 NIH_MGC_67 H... 1229 0.0
gi|5664763|gb|AI928864.1|AI928864 au64c05.x1 Schneider feta... 1207 0.0
gi|13913479|gb|BG682082.1|BG682082 602630059F1 NCI_CGAP_Skn... 1191 0.0
gi|12417863|gb|BG028768.1|BG028768 602292961F1 NIH_MGC_86 H... 1180 0.0
gi|12797240|emb|AL533747.1|AL533747 AL533747 LTI_FL013_FBrn... 1172 0.0
gi|12412351|gb|BG025595.1|BG025595 602274520F1 NIH_MGC_85 H... 1154 0.0
gi|2716956|gb|AA707038.1|AA707038 zj32c08.s1 Soares_fetal_I... 1120 0.0
gi|10203449|gb|BE782251.1|BE782251 601466684F1 NIH_MGC_67 H... 1102 0.0
gi|7376813|gb|AW630023.1|AW630023 hh74c04.y1 NCI_CGAP_GU1 H... 1102 0.0
gi|2357785|gb|AA579601.1|AA579601 nm71h09.s1 NCI_CGAP_Co9 H... 1086 0.0
gi|10740475|gb|BF032763.1|BF032763 601453471F1 NIH_MGC_66 H... 1084 0.0
gi|3253464|gb|AI032767.1|AI032767 ox13h06.x1 Soares_fetal_I... 1070 0.0
gi|13968664|gb|BG699891.1|BG699891 602681245F1 NIH_MGC_95 H... 1051 0.0

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gi|2397741|gb|AA586927.1|AA586927 nn68g03.s1 NCI_CGAP_Lar1 ... 1013 0.0
gi|11592515|gb|BF509217.1|BF509217 UI-H-BI4-aov-h-02-0-UI.s... 1001 0.0
gi|5664992|gb|AI929028.1|AI929028 au64c05.y1 Schneider feta... 985 0.0
gi|2908208|gb|AA834609.1|AA834609 od64c08.s1 NCI_CGAP_GCB1 ... 981 0.0
gi|6589783|gb|AW246790.1|AW246790 2822178.3prime NIH_MGC_7 ... 975 0.0
gi|13987461|gb|BG709280.1|BG709280 602674673F1 NIH_MGC_96 H... 954 0.0
gi|6086780|gb|AW118196.1|AW118196 xd91b01.x1 Soares_NFL_T_G... 950 0.0
gi|13987880|gb|BG709491.1|BG709491 602674765F1 NIH_MGC_96 H... 938 0.0
gi|1633828|gb|AA088298.1|AA088298 zl84d09.r1 Stratagene col... 934 0.0
gi|2875181|gb|AA806431.1|AA806431 oc23a07.s1 NCI_CGAP_GCB1 ... 910 0.0
```

>gi|10439230|dbj|BAB15467.1| unnamed protein product [Homo sapiens]

EST search: testis, melanotic melanoma, adenocarcinoma (cellline)

Sequences producing significant alignments: (bits) Value

```
gi|13999456|gb|BG720269.1|BG720269 602692330F1 NIH_MGC_97 H... 1217 0.0
gi|11975300|gb|BF689892.1|BF689892 602186442F1 NIH_MGC_49 H... 1209 0.0
gi|10350124|gb|BE891116.1|BE891116 601432231F1 NIH_MGC_72 H... 1118 0.0
gi|10161479|gb|BE747487.1|BE747487 601573861F1 NIH_MGC_9 Ho... 965 0.0
```

>gi|14764177|ref|XP_044864.1| hypothetical protein FLJ10462 [Homo sapiens]

EST search: neuroblastoma; skin; lung

Sequences producing significant alignments: (bits) Value

```
gi|12792604|emb|AL529111.1|AL529111 AL529111 LTI_NFL001_NBC... 1663 0.0
gi|14052499|gb|BG741846.1|BG741846 602634860F1 NCI_CGAP_Skn... 1562 0.0
gi|12792603|emb|AL529110.1|AL529110 AL529110 LTI_NFL001_NBC... 1505 0.0
gi|13544215|gb|BG545550.1|BG545550 602572801F1 NIH_MGC_77 H... 1417 0.0
gi|13459313|gb|BG497796.1|BG497796 602543069F1 NIH_MGC_60 H... 1310 0.0
gi|13983654|gb|BG707372.1|BG707372 602672776F1 NIH_MGC_96 H... 1239 0.0
gi|4684870|gb|AI633540.1|AI633540 th68d07.x1 Soares_NhHMPu... 1229 0.0
gi|13342208|gb|BG435702.1|BG435702 602506802F1 NIH_MGC_79 H... 1207 0.0
gi|10700212|gb|BE999936.1|BE999936 7h20b10.x1 NCI_CGAP_Co16... 1197 0.0
gi|9810737|gb|BE567017.1|BE567017 601341163F1 NIH_MGC_53 Ho... 1180 0.0
gi|11985103|gb|BF699695.1|BF699695 602127115F1 NIH_MGC_56 H... 1160 0.0
gi|13521358|gb|BG529821.1|BG529821 602558905F1 NIH_MGC_61 H... 1120 0.0
gi|10997231|dbj|AU136692.1|AU136692 AU136692 PLACE1 Homo sa... 1072 0.0
gi|2207965|gb|AA479409.1|AA479409 zv21g08.r1 Soares_NhHMPu... 1057 0.0
gi|5631452|gb|AI911597.1|AI911597 wc86a01.x1 NCI_CGAP_Co3 H... 1029 0.0
gi|2207864|gb|AA479308.1|AA479308 zv21g08.s1 Soares_NhHMPu... 932 0.0
gi|5865542|gb|AW016785.1|AW016785 UI-H-BI0p-abm-g-01-0-UI.s... 926 0.0
```

>gi|14041699|emb|CAC38443.1| dJ1033B10.9.2 (FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like, isoform 2) [Homo sapiens]

97% identical to DHB8; EST search not performed: only 180 Kbp available

>gi|14041946|dbj|BAB55045.1| (AK027337) unnamed protein product

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EST search with poor annotated entry: weak similarities with cDNAs expressed in adrenal gland, colon tumor, liver, spleen,lung

Sequences producing significant alignments:	(bits)	Value
gi 10721718 gb AV704400.1 AV704400 AV704400 ADB Homo sapi... 1059	0.0	
gi 8165991 gb AW974788.1 AW974788 EST386893 MAGE resequence... 1057	0.0	
gi 1424282 gb W91890.1 W91890 zh47a06.r1 Soares_fetal_liver... 1029	0.0	
gi 10940429 gb BF110739.1 BF110739 7n56b09.x1 NCI_CGAP_Lu24... 971	0.0	
gi 12613045 gb BG119539.1 BG119539 602347238F1 NIH_MGC_90 H... 950	0.0	
gi 2657822 gb AA677300.1 AA677300 zj61f10.s1 Soares_fetal_l... 900	0.0	

putative SDRs identified with no obvious annotation as SDRs in NCBI database and/or referenced Medline/PubMed-link

>gi|11435147|ref|XP_006732.1| retinol dehydrogenase 5 (11-cis and 9-cis) [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 8908990 gb BE221672.1 BE221672 hu27e10.x1 NCI_CGAP_Mel15... 1146	0.0	
gi 4900121 gb AI688827.1 AI688827 wd41d07.x1 SoaresNFL_T_G... 969	0.0	
gi 4618930 gb AI609763.1 AI609763 tf83a04.x1 NCI_CGAP_Brn23... 959	0.0	
gi 11081688 gb BF195132.1 BF195132 7n15f01.x1 NCI_CGAP_Brn2... 950	0.0	
gi 4264406 gb AI418475.1 AI418475 tf74h03.x1 NCI_CGAP_Brn23... 946	0.0	
gi 14292293 gb BG911817.1 BG911817 602810064F1 NCI_CGAP_Brn... 938	0.0	
gi 11593828 gb BF510530.1 BF510530 UI-H-BI4-apa-e-11-0-UI.s... 846	0.0	
gi 4114767 gb AI363146.1 AI363146 qy55a02.x1 NCI_CGAP_Brn23... 799	0.0	
gi 5854635 gb AW005857.1 AW005857 wz80d08.x1 NCI_CGAP_Gas4 ... 797	0.0	
gi 6661708 gb AW274678.1 AW274678 xv32d08.x1 SoaresNFL_T_G... 783	0.0	
gi 2525787 gb AA621911.1 AA621911 nq30b08.s1 NCI_CGAP_Co10 ... 781	0.0	
gi 5527702 gb AI863595.1 AI863595 wj18h11.x1 NCI_CGAP_Kid12... 688	0.0	
gi 1190064 gb N48898.1 N48898 yy77e08.s1 Soares_multiple_sc... 688	0.0	
gi 2505366 gb AA618161.1 AA618161 nq14d10.s1 NCI_CGAP_Thy1 ... 686	0.0	
gi 2656640 gb AA680173.1 AA680173 zi11b06.s1 Soares_fetal_l... 684	0.0	
gi 5396293 gb AI809727.1 AI809727 wh77a07.x1 NCI_CGAP CLL1 ... 682	0.0	
gi 3279324 gb AI040130.1 AI040130 ox08h01.x1 Soares_fetal_l... 664	0.0	
gi 1448549 gb AA004494.1 AA004494 zh87b01.r1 Soares_fetal_l... 650	0.0	
gi 1018746 gb H63945.1 H63945 yr55b01.s1 Soares fetal liver... 632	e-179	
gi 1716962 gb AA147453.1 AA147453 zj51h03.r1 Soares_pregnant... 613	e-173	
gi 1524527 gb AA046629.1 AA046629 zk62h02.r1 Soares_pregnant... 611	e-172	
gi 1188267 gb N47101.1 N47101 yy85f02.s1 Soares_multiple_sc... 601	e-169	

>gi|13655317|ref|XP_007380.2| CGI-86 protein [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi|12908926|emb|AL561466.1|AL561466 AL561466 LTI_NFL010_BC2... 1475 0.0
 gi|12908868|emb|AL561437.1|AL561437 AL561437 LTI_NFL010_BC2... 1457 0.0
 gi|13705885|gb|BG184198.1|BG184198 RST3119 Athersys RAGE Li... 1455 0.0
 gi|10161043|gb|BE747051.1|BE747051 601580610F1 NIH_MGC_9 Ho... 1382 0.0
 gi|9141043|gb|BE267452.1|BE267452 601189745F2 NIH_MGC_7 Horn... 1285 0.0
 gi|14080921|gb|BG770268.1|BG770268 602744858F1 NIH_MGC_49 H... 1281 0.0
 gi|3308715|gb|AI052724.1|AI052724 oz27a12.x1 Soares_total_f... 1227 0.0
 gi|6300903|gb|AW161870.1|AW161870 au71a04.x1 Schneider feta... 1215 0.0
 gi|13583649|gb|BG575996.1|BG575996 602597341F1 NIH_MGC_87 H... 1189 0.0
 gi|13135151|gb|BG328713.1|BG328713 602427988F1 NIH_MGC_15 H... 1181 0.0
 gi|12337285|gb|BF970070.1|BF970070 602272338F1 NIH_MGC_84 H... 1164 0.0
 gi|11649289|gb|BF575655.1|BF575655 602133057F1 NIH_MGC_81 H... 1162 0.0
 gi|10149412|gb|BE735420.1|BE735420 601304204F1 NIH_MGC_39 H... 1160 0.0
 gi|13134589|gb|BG328151.1|BG328151 602427216F1 NIH_MGC_15 H... 1152 0.0
 gi|5633042|gb|AI913268.1|AI913268 wa10f08.x1 NCI_CGAP_Kid11... 1148 0.0
 gi|13405005|gb|BG472730.1|BG472730 602514555F1 NIH_MGC_16 H... 1114 0.0
 gi|13411959|gb|BG479680.1|BG479680 602527142F1 NIH_MGC_21 H... 1102 0.0
 gi|10888750|gb|BF106224.1|BF106224 601823412F1 NIH_MGC_77 H... 1098 0.0
 gi|10700778|gb|BF000503.1|BF000503 7h32a01.x1 NCI_CGAP_Co16... 1084 0.0
 gi|6709918|gb|AW300318.1|AW300318 xs59g06.x1 NCI_CGAP_Kid11... 1078 0.0
 gi|11947563|gb|BF673668.1|BF673668 602136388F1 NIH_MGC_83 H... 1072 0.0
 gi|11685208|gb|BF592884.1|BF592884 7j95h06.x1 NCI_CGAP_GC6 ... 1070 0.0
 gi|10984835|gb|BF115433.1|BF115433 7n81h06.x1 NCI_CGAP_Ov18... 1070 0.0
 gi|13544202|gb|BG545537.1|BG545537 602572781F1 NIH_MGC_77 H... 1061 0.0
 gi|13404427|gb|BG472241.1|BG472241 602513753F1 NIH_MGC_16 H... 1059 0.0
 gi|11951687|gb|BF677792.1|BF677792 602085496F1 NIH_MGC_83 H... 1039 0.0
 gi|10940810|gb|BF111120.1|BF111120 7n43g10.x1 NCI_CGAP_Lu24... 1027 0.0
 gi|13137281|gb|BG330843.1|BG330843 602431480F1 NIH_MGC_18 H... 1017 0.0
 gi|13971790|gb|BG701448.1|BG701448 602682670F1 NIH_MGC_95 H... 1013 0.0
 gi|11952455|gb|BF678560.1|BF678560 602086022F1 NIH_MGC_83 H... 1011 0.0
 gi|11450749|gb|BF438232.1|BF438232 7q68g12.x1 NCI_CGAP_Lu24... 1009 0.0
 gi|11060866|gb|BF182723.1|BF182723 601809222F1 NIH_MGC_18 H... 1005 0.0
 gi|6197433|gb|AW149537.1|AW149537 xf39b12.x1 NCI_CGAP_Bm50... 997 0.0
 gi|9510747|gb|BE464972.1|BE464972 hv76a11.x1 NCI_CGAP_Lu24 ... 995 0.0
 gi|13290415|gb|BG396967.1|BG396967 602433879F1 NIH_MGC_20 H... 991 0.0
 gi|9333920|gb|BE388555.1|BE388555 601281843F1 NIH_MGC_44 Ho... 975 0.0
 gi|3056175|gb|AA916783.1|AA916783 on10d05.s1 NCI_CGAP_Lu5 H... 973 0.0
 gi|10209987|gb|BE788800.1|BE788800 601475705F1 NIH_MGC_68 H... 965 0.0
 gi|6710858|gb|AW301181.1|AW301181 xs57d11.x1 NCI_CGAP_Kid11... 959 0.0
 gi|9335147|gb|BE389782.1|BE389782 601282967F1 NIH_MGC_44 Ho... 957 0.0
 gi|4985638|gb|AI697738.1|AI697738 we16g07.x1 NCI_CGAP_Lu24 ... 954 0.0
 gi|9334997|gb|BE389632.1|BE389632 601283343F1 NIH_MGC_44 Ho... 952 0.0
 gi|11649406|gb|BF575694.1|BF575694 602135311F1 NIH_MGC_81 H... 942 0.0
 gi|1371301|gb|W63721.1|W63721 zc58g09.r1 Soares_parathyroid... 934 0.0
 gi|10821341|gb|BF062431.1|BF062431 7h59a01.x1 NCI_CGAP_Co16... 926 0.0
 gi|9126816|gb|BE256444.1|BE256444 601108430F1 NIH_MGC_16 Ho... 924 0.0
 gi|11979410|gb|BF694002.1|BF694002 602082590F1 NIH_MGC_81 H... 920 0.0
 gi|9123725|gb|BE253566.1|BE253566 601108683F1 NIH_MGC_16 Ho... 914 0.0
 gi|5424673|gb|AI813458.1|AI813458 wj06f03.x1 NCI_CGAP_Kid12... 912 0.0
 gi|3419256|gb|AI082464.1|AI082464 os71e10.x1 NCI_CGAP_GC2 H... 912 0.0
 gi|13326319|gb|BG419813.1|BG419813 602453265F1 NIH_MGC_14 H... 906 0.0
 gi|11945543|gb|BF671648.1|BF671648 602151504F1 NIH_MGC_81 H... 902 0.0
 gi|5934152|gb|AW058513.1|AW058513 wx21h07.x1 NCI_CGAP_Bm... 900 0.0
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>gi|12734537|ref|XP_005309.2| 2,4-dienoyl CoA reductase 1 precursor [Homo sapiens]

EST Search:

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[Homo sapiens]

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>gi|5531815|gb|AAD44482.1| steroid dehydrogenase homolog [Homo sapiens]

EST Search:

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 gi|4969797|gb|AI692457.1|AI692457 wd70f09.x1 NCI_CGAP_Lu24 ... 803 0.0
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gi 10721512 gb AV704193.1 AV704193 AV704193 ADB Homo sapie...	1033	0.0
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gi|11647948|gb|BF574236.1|BF574236 602131406F1 NIH_MGC_81 H... 952 0.0
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>gi|6523809|gb|AAF14864.1|AF113123_1 carbonyl reductase [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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 gi|3241643|gb|AI026030.1|AI026030 ow03f06.s1 Soares_parathy... 890 0.0
 gi|10920186|dbj|AV762338.1|AV762338 AV762338 MDS Homo sapie... 878 0.0
 gi|1471524|gb|AA010478.1|AA010478 zi09e01.r1 Soares_fetal_l... 878 0.0
 gi|2269399|gb|AA527330.1|AA527330 ng36c09.s1 NCI_CGAP_Co3 H... 870 0.0
 gi|12161980|gb|BF822251.1|BF822251 MR1-RT0041-051200-007-f1... 862 0.0
 gi|9175770|gb|BE304542.1|BE304542 601105911F1 NIH_MGC_15 Ho... 854 0.0
 gi|1959201|gb|AA306873.1|AA306873 EST177798 Jurkat T-cells ... 848 0.0

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```
gi|3934019|gb|AI291245.1|AI291245 qm11c01.x1 NCI_CGAP_Lu5 H... 844 0.0
gi|2842062|gb|AA782731.1|AA782731 aj08a05.s1 Soares_parathy... 835 0.0
gi|13916648|gb|BG685251.1|BG685251 602637158F1 NIH_MGC_48 H... 833 0.0
gi|3086142|gb|AA931756.1|AA931756 oo77f06.s1 NCI_CGAP_Kid5 ... 827 0.0
gi|1349991|gb|W51877.1|W51877 zc36c10.s1 Soares_senescent_f... 827 0.0
gi|14001369|gb|BG722182.1|BG722182 602698423F1 NIH_MGC_97 H... 825 0.0
gi|3154538|gb|AA977092.1|AA977092 oq24a03.s1 NCI_CGAP_GC4 H... 819 0.0
gi|2113245|gb|AA429946.1|AA429946 zw67f12.s1 Soares_testis_... 819 0.0
gi|11970016|gb|BF684608.1|BF684608 602140946F1 NIH_MGC_46 H... 815 0.0
gi|14564968|gb|BI114067.1|BI114067 602861166F2 NIH_MGC_17 H... 813 0.0
gi|1696541|gb|AA135492.1|AA135492 zo28h02.s1 Stratagene col... 805 0.0
gi|10159931|gb|BE745939.1|BE745939 601573574F1 NIH_MGC_9 Ho... 801 0.0
```

>gi|11360148|pir||T46363 hypothetical protein DKFZp434O0916.1 - human
(fragment)

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 7848800 gb AW796930.1 AW796930 CM3-UM0034-230300-126-d05...	38	2.8
gi 7844653 gb AW792874.1 AW792874 CM3-UM0001-280100-082-e12...	38	2.8
gi 7111080 gb AW466324.1 AW466324 bbc1g1b52 Neuronal Differ...	38	2.8
gi 772618 gb R19008.1 R19008 yg26d09.r1 Soares_infant brain...	38	2.8

>gi|7023407|dbj|BAA91953.1| unnamed protein product [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 10220190 gb BE798992.1 BE798992 601583126F1 NIH_MGC_7 Ho...	1487	0.0
gi 9149748 gb BE274802.1 BE274802 601122492F1 NIH_MGC_20 Ho...	1483	0.0
gi 10158478 gb BE744486.1 BE744486 601576764F1 NIH_MGC_9 Ho...	1433	0.0
gi 15018843 gb BI334186.1 BI334186 602997649F1 NIH_MGC_12 H...	1427	0.0
gi 10155434 gb BE741442.1 BE741442 601594426F1 NIH_MGC_9 Ho...	1392	0.0
gi 12767656 gb BG257840.1 BG257840 602377359F1 NIH_MGC_92 H...	1360	0.0
gi 2555545 gb AA632131.1 AA632131 np74e04.s1 NCI_CGAP_Br2 H...	1344	0.0
gi 13961948 gb BG696620.1 BG696620 602658918F1 NCI_CGAP_Skn...	1340	0.0
gi 13293198 gb BG399750.1 BG399750 602441351F1 NIH_MGC_75 H...	1340	0.0
gi 13343333 gb BG436827.1 BG436827 602488812F1 NIH_MGC_18 H...	1336	0.0
gi 15020179 gb BI335522.1 BI335522 602997109F1 NIH_MGC_12 H...	1318	0.0
gi 12616196 gb BG122687.1 BG122687 602351815F1 NIH_MGC_90 H...	1306	0.0
gi 5848066 gb AW001150.1 AW001150 wu25a06.x1 Soares_Dieckgr...	1287	0.0
gi 9807602 gb BE563882.1 BE563882 601335069F1 NIH_MGC_39 Ho...	1283	0.0
gi 5544472 gb AI870504.1 AI870504 wl74d11.x1 NCI_CGAP_Brn25...	1275	0.0
gi 14620794 gb BI160793.1 BI160793 602864883F1 NIH_MGC_42 H...	1249	0.0
gi 11972158 gb BF686750.1 BF686750 602143895F1 NIH_MGC_46 H...	1249	0.0
gi 3887481 gb AI268314.1 AI268314 qm04c02.x1 NCI_CGAP_Lu5 H...	1241	0.0
gi 10206517 gb BE785319.1 BE785319 601474695F1 NIH_MGC_68 H...	1231	0.0
gi 10996420 dbj AU135881.1 AU135881 AU135881 PLACE1 Homo sa...	1227	0.0
gi 6588855 gb AW245862.1 AW245862 2822884.5prime NIH_MGC_7 ...	1140	0.0
gi 3425727 gb AI087304.1 AI087304 oz77h11.x1 Soares_senesce...	1136	0.0
gi 3400045 gb AI073401.1 AI073401 ov46a12.x1 Soares_testis_...	1128	0.0

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gi|3601194|gb|AI131178.1|AI131178 qc15d06.x1 Soares_fetal_h... 1118 0.0
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 gi|9323511|gb|BE378146.1|BE378146 601237876F1 NIH_MGC_44 Ho... 1084 0.0
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 gi|6947123|gb|AW419191.1|AW419191 hb73d11.x1 NCI_CGAP_Ut2 H... 1039 0.0
 gi|1941184|gb|AA293161.1|AA293161 zt55e02.s1 Soares_ovary t... 1029 0.0
 gi|9260951|gb|BE349176.1|BE349176 ht49c06.x1 NCI_CGAP_Mel15... 1015 0.0
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 gi|13793809|gb|BG656400.1|BG656400 ib36h12.x1 HR85 islet Ho... 1009 0.0
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 gi|1382848|gb|W72175.1|W72175 zd61e02.s1 Soares_fetal_heart... 995 0.0
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 gi|2879104|gb|AA809698.1|AA809698 nk96e07.s1 NCI_CGAP_Co3 H... 983 0.0
 gi|2563616|gb|AA639837.1|AA639837 nq85a11.s1 NCI_CGAP_Co9 H... 983 0.0
 gi|6026748|gb|AW071823.1|AW071823 ws54b01.x1 NCI_CGAP_Brn25... 981 0.0
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 gi|4070443|gb|AI333884.1|AI333884 qq17e01.x1 Soares_NhHMPu... 928 0.0
 gi|3958752|gb|AI299098.1|AI299098 qn14e10.x1 NCI_CGAP_Lu5 H... 912 0.0
 gi|2732328|gb|AA719229.1|AA719229 ah45g05.s1 Soares_testis... 912 0.0
 gi|2878736|gb|AA809330.1|AA809330 ob70c08.s1 NCI_CGAP_GCB1 ... 910 0.0
 gi|1153479|gb|N33080.1|N33080 yy33d10.s1 Soares_melanocyte ... 908 0.0
 gi|5513052|gb|AI859436.1|AI859436 wm11e11.x1 NCI_CGAP_Ut4 H... 906 0.0
 gi|5447444|gb|AI826773.1|AI826773 wk56a11.x1 NCI_CGAP_Pr22 ... 892 0.0
 gi|3241643|gb|AI026030.1|AI026030 ow03f06.s1 Soares_parathy... 890 0.0
 gi|10920186|dbj|AV762338.1|AV762338 AV762338 MDS Homo sapi... 878 0.0
 gi|1471524|gb|AA010478.1|AA010478 zi09e01.r1 Soares_fetal_l... 878 0.0
 gi|2269399|gb|AA527330.1|AA527330 ng36c09.s1 NCI_CGAP_Co3 H... 870 0.0
 gi|12161980|gb|BF822251.1|BF822251 MR1-RT0041-051200-007-f1... 862 0.0
 gi|9175770|gb|BE304542.1|BE304542 601105911F1 NIH_MGC_15 Ho... 854 0.0
 gi|1959201|gb|AA306873.1|AA306873 EST177798 Jurkat T-cells ... 848 0.0
 gi|3934019|gb|AI291245.1|AI291245 qm11c01.x1 NCI_CGAP_Lu5 H... 844 0.0
 gi|2842062|gb|AA782731.1|AA782731 aj08a05.s1 Soares_parathy... 835 0.0
 gi|13916648|gb|BG685251.1|BG685251 602637158F1 NIH_MGC_48 H... 833 0.0
 gi|3086142|gb|AA931756.1|AA931756 oo77f06.s1 NCI_CGAP_Kid5 ... 827 0.0
 gi|1349991|gb|W51877.1|W51877 zc36c10.s1 Soares_senescent_f... 827 0.0
 gi|14001369|gb|BG722182.1|BG722182 602698423F1 NIH_MGC_97 H... 825 0.0
 gi|3154538|gb|AA977092.1|AA977092 oq24a03.s1 NCI_CGAP_GC4 H... 819 0.0
 gi|2113245|gb|AA429946.1|AA429946 zw67f12.s1 Soares_testis... 819 0.0
 gi|11970016|gb|BF684608.1|BF684608 602140946F1 NIH_MGC_46 H... 815 0.0
 gi|14564968|gb|BI114067.1|BI114067 602861166F2 NIH_MGC_17 H... 813 0.0
 gi|1696541|gb|AA135492.1|AA135492 zo28h02.s1 Stratagene col... 805 0.0
 gi|10159931|gb|BE745939.1|BE745939 601573574F1 NIH_MGC_9 Ho... 801 0.0

>gi|14734800|ref|XP_002640.3| peroxisomal trans 2-enoyl CoA reductase;
putative short chain al [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 12789234 emb AL525741.1 AL525741 AL525741 LTI_NFL003_NBC...	1826	0.0

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gi|12791177|emb|AL527684.1|AL527684 AL527684 LTI_NFL003_NBC... 1663 0.0
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gi|14053003|gb|BG742350.1|BG742350 602631722F1 NCI_CGAP_Skn... 1503 0.0
gi|14045131|gb|BG774814.1|BG774814 602662684F1 NIH_MGC_21 H... 1415 0.0
gi|14052853|gb|BG742200.1|BG742200 602634087F1 NCI_CGAP_Skn... 1396 0.0
gi|9873450|dbj|AV652436.1|AV652436 AV652436 GLC Homo sapien... 1348 0.0
gi|12786797|emb|AL523304.1|AL523304 AL523304 LTI_NFL003_NBC... 1336 0.0
gi|13722475|gb|BG200900.1|BG200900 RST20108 Athersys RAGE L... 1336 0.0
gi|12911098|emb|AL562558.1|AL562558 AL562558 LTI_NFL003_NBC... 1166 0.0
gi|5232357|gb|AI765848.1|AI765848 wi85c03.x1 NCI_CGAP_Kid12... 1134 0.0
gi|10914602|dbj|AV756754.1|AV756754 AV756754 BM Homo sapien... 1100 0.0
gi|8907537|gb|BE220231.1|BE220231 hv69f02.x1 NCI_CGAP_Lu24 ... 1017 0.0
gi|14053002|gb|BG742349.1|BG742349 602631721F1 NCI_CGAP_Skn... 995 0.0
gi|10938068|gb|BF108369.1|BF108369 7n62f05.x1 NCI_CGAP_Lu24... 993 0.0
gi|4303253|gb|AI435448.1|AI435448 th94e11.x1 Soares_NSF_F8_... 906 0.0
gi|11363688|gb|BF382385.1|BF382385 601815316F2 NIH_MGC_56 H... 896 0.0
gi|9792594|gb|BE550902.1|BE550902 7b65g01.x1 NCI_CGAP_Lu24 ... 894 0.0
gi|9184025|gb|BE300277.1|BE300277 600944051T1 NIH_MGC_17 Ho... 858 0.0
gi|9155968|gb|BE280956.1|BE280956 601155875F1 NIH_MGC_21 Ho... 852 0.0
gi|12041930|gb|BF726019.1|BF726019 bx23a05.y1 Human Iris cD... 844 0.0
gi|12135102|gb|BF806113.1|BF806113 MR1-CI0183-071100-001-f0... 841 0.0
gi|4312182|gb|AI458176.1|AI458176 tj94c11.x1 NCI_CGAP_Lu24 ... 807 0.0

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SDRs identified with "SDR region" mostly by automated alignment (BLAST Domain) and unreviewed description in NCBI database (identification might be " putative" SDR or "putative" protein); substrate and/or function might be unknown. Exceptions may be for example known hydroxysteroid dehydrogenases like 17-beta HSD1-10 and 11-beta-HSD1-2 and retinol/retinal dehydrogenases

>gi|65913|pir||DEHUE7 estradiol 17beta-dehydrogenase (EC 1.1.1.62) type 1 -
human

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 12877696 emb AL545215.1 AL545215 AL545215 LTI_NFL006_PL2... 1663	0.0	
gi 12878160 emb AL545678.1 AL545678 AL545678 LTI_NFL006_PL2... 1651	0.0	
gi 12889399 emb AL551445.1 AL551445 AL551445 LTI_NFL006_PL2... 1641	0.0	
gi 12893008 emb AL553301.1 AL553301 AL553301 LTI_NFL006_PL2... 1639	0.0	
gi 12875567 emb AL543089.1 AL543089 AL543089 LTI_NFL006_PL2... 1618	0.0	
gi 12894623 emb AL554134.1 AL554134 AL554134 LTI_NFL006_PL2... 1564	0.0	
gi 12880090 emb AL546712.1 AL546712 AL546712 LTI_NFL006_PL2... 1524	0.0	
gi 12884123 emb AL548779.1 AL548779 AL548779 LTI_NFL006_PL2... 1451	0.0	
gi 12882682 emb AL548045.1 AL548045 AL548045 LTI_NFL006_PL2... 1417	0.0	
gi 12928450 emb AL571296.1 AL571296 AL571296 LTI_NFL006_PL2... 1300	0.0	
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gi 11000660 dbj AU139139.1 AU139139 AU139139 PLACE1 Homo sa... 1215	0.0	
gi 12876594 emb AL544115.1 AL544115 AL544115 LTI_NFL006_PL2... 1191	0.0	
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gi 10996612 dbj AU136073.1 AU136073 AU136073 PLACE1 Homo sa... 1185	0.0	
gi 12935757 emb AL575009.1 AL575009 AL575009 LTI_NFL006_PL2... 1176	0.0	
gi 12929750 emb AL571950.1 AL571950 AL571950 LTI_NFL006_PL2... 1160	0.0	
gi 11000929 dbj AU139408.1 AU139408 AU139408 PLACE1 Homo sa... 1154	0.0	
gi 12925425 emb AL569763.1 AL569763 AL569763 LTI_NFL006_PL2... 1118	0.0	
gi 12938593 emb AL576443.1 AL576443 AL576443 LTI_NFL006_PL2... 1110	0.0	
gi 12874250 emb AL542321.1 AL542321 AL542321 LTI_FL002_PL1 ... 1078	0.0	
gi 12887536 emb AL550503.1 AL550503 AL550503 LTI_NFL006_PL2... 1023	0.0	
gi 12927925 emb AL571031.1 AL571031 AL571031 LTI_NFL006_PL2... 983	0.0	
gi 12884042 emb AL548739.1 AL548739 AL548739 LTI_NFL006_PL2... 981	0.0	
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gi 12882968 emb AL548193.1 AL548193 AL548193 LTI_NFL006_PL2... 952	0.0	
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gi 10996163 dbj AU135624.1 AU135624 AU135624 PLACE1 Homo sa... 896	0.0	
gi 11000650 dbj AU139129.1 AU139129 AU139129 PLACE1 Homo sa... 894	0.0	
gi 11000302 dbj AU138781.1 AU138781 AU138781 PLACE1 Homo sa... 894	0.0	
gi 10999181 dbj AU137660.1 AU137660 AU137660 PLACE1 Homo sa... 894	0.0	
gi 11000400 dbj AU138879.1 AU138879 AU138879 PLACE1 Homo sa... 886	0.0	
gi 10941914 gb BF112224.1 BF112224 7I42c05.x1 Soares_NSF_F8...	825	0.0
gi 12872814 emb AL541595.1 AL541595 AL541595 LTI_FL002_PL1 ... 799	0.0	
gi 10941804 gb BF112114.1 BF112114 7I40e05.x1 Soares_NSF_F8...	779	0.0
gi 10999521 dbj AU138000.1 AU138000 AU138000 PLACE1 Homo sa... 696	0.0	
gi 12939576 emb AL576938.1 AL576938 AL576938 LTI_NFL006_PL2... 686	0.0	
gi 10997013 dbj AU136474.1 AU136474 AU136474 PLACE1 Homo sa... 682	0.0	
gi 1571801 dbj C17094.1 C17094 C17094 Clontech human aorta ... 682	0.0	
gi 1722365 gb AA150854.1 AA150854 zI44b07.r1 Soares_pregnan...	666	0.0
gi 1579212 dbj C17609.1 C17609 C17609 Human placenta cDNA (... 660	0.0	
gi 11018663 dbj AU157142.1 AU157142 AU157142 PLACE1 Homo sa... 652	0.0	

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gi|2718881|gb|AA708963.1|AA708963 zl58g02.s1 Soares_pregnant... 648 0.0
 gi|12875835|emb|AL543357.1|AL543357 AL543357 LTI_NFL006_PL2... 626 e-
 177
 gi|10941920|gb|BF112230.1|BF112230 7142d05.x1 Soares_NSF_F8... 618 e-
 174
 gi|2715031|gb|AA705113.1|AA705113 zj94h11.s1 Soares_fetal_l... 597 e-
 168
 gi|12442104|gb|BG002508.1|BG002508 MR3-GN0186-171100-005-e0... 595 e-
 167
 gi|1722257|gb|AA150545.1|AA150545 zl44b07.s1 Soares_pregnant... 593 e-
 167
 gi|12396831|gb|BF990506.1|BF990506 RC0-GN0133-261000-031-c0... 585 e-
 164
 gi|1722312|gb|AA150800.1|AA150800 zl46b07.r1 Soares_pregnant... 581 e-
 163
 gi|4435924|gb|AI521789.1|AI521789 ti77d11.x1 NCI_CGAP_Kid11... 579 e-
 163
 gi|12923868|emb|AL568983.1|AL568983 AL568983 LTI_FL002_PL1 ... 575 e-
 161
 gi|12926714|emb|AL570422.1|AL570422 AL570422 LTI_NFL006_PL2... 557 e-
 156
 gi|4665448|gb|AI628648.1|AI628648 ty77e09.x1 NCI_CGAP_Kid11... 553 e-
 155
 gi|848714|gb|R74344.1|R74344 yl01f08.s1 Soares breast 2NbHB... 551 e-
 154

>gi|4504503|ref|NP_002144.1| hydroxysteroid (17-beta) dehydrogenase 2 [Homo sapiens]

EST Search:

Sequences producing significant alignments: (bits) Value

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gi 12928176 emb AL571159.1 AL571159 AL571159 LTI_NFL006_PL2... 1832 0.0
gi 12938929 emb AL576614.1 AL576614 AL576614 LTI_NFL006_PL2... 1818 0.0
gi 12891054 emb AL552292.1 AL552292 AL552292 LTI_NFL006_PL2... 1810 0.0
gi 12879139 emb AL546227.1 AL546227 AL546227 LTI_NFL006_PL2... 1806 0.0
gi 12890884 emb AL552206.1 AL552206 AL552206 LTI_NFL006_PL2... 1764 0.0
gi 12936979 emb AL575629.1 AL575629 AL575629 LTI_NFL006_PL2... 1760 0.0
gi 12893833 emb AL553729.1 AL553729 AL553729 LTI_NFL006_PL2... 1746 0.0
gi 12927335 emb AL570735.1 AL570735 AL570735 LTI_NFL006_PL2... 1719 0.0
gi 12877918 emb AL545437.1 AL545437 AL545437 LTI_NFL006_PL2... 1719 0.0
gi 12937110 emb AL575695.1 AL575695 AL575695 LTI_NFL006_PL2... 1673 0.0
gi 12928206 emb AL571174.1 AL571174 AL571174 LTI_NFL006_PL2... 1631 0.0
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gi 12877944 emb AL545463.1 AL545463 AL545463 LTI_NFL006_PL2... 1582 0.0
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gi 12940371 emb AL577339.1 AL577339 AL577339 LTI_NFL006_PL2... 1459 0.0
gi 12939042 emb AL576670.1 AL576670 AL576670 LTI_NFL006_PL2... 1435 0.0

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gi|13580329|gb|BG572676.1|BG572676 602593783F1 NIH_MGC_79 H... 1425 0.0
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gi|13575119|gb|BG567466.1|BG567466 602585994F1 NIH_MGC_76 H... 1354 0.0
gi|11000555|dbj|AU139034.1|AU139034 AU139034 PLACE1 Homo sa... 1338 0.0
gi|13670494|gb|BG619123.1|BG619123 602616490F1 NIH_MGC_79 H... 1332 0.0
gi|9719951|gb|BE512678.1|BE512678 601171639F1 NIH_MGC_15 Ho... 1310 0.0
gi|10995811|dbj|AU135272.1|AU135272 AU135272 PLACE1 Homo sa... 1294 0.0
gi|13519989|gb|BG528452.1|BG528452 602579896F1 NIH_MGC_60 H... 1279 0.0
gi|12940459|emb|AL577384.1|AL577384 AL577384 LTI_NFL006_PL2... 1191 0.0
gi|9869431|dbj|AV648417.1|AV648417 AV648417 GLC Homo sapien... 1148 0.0
gi|10286850|dbj|AV684987.1|AV684987 AV684987 GKC Homo sapie... 1138 0.0
gi|9871386|dbj|AV650372.1|AV650372 AV650372 GLC Homo sapien... 1128 0.0
gi|8141093|gb|AW951420.1|AW951420 EST363490 MAGE resequence... 1094 0.0
gi|9874839|dbj|AV653825.1|AV653825 AV653825 GLC Homo sapien... 1076 0.0
gi|9812898|gb|BE569178.1|BE569178 601338993F2 NIH_MGC_53 Ho... 1037 0.0
gi|12041605|gb|BF725694.1|BF725694 bx18g03.y1 Human Iris cD... 1013 0.0
gi|12940352|emb|AL577329.1|AL577329 AL577329 LTI_NFL006_PL2... 999 0.0
gi|10300921|dbj|AV698950.1|AV698950 AV698950 GKC Homo sapie... 989 0.0
gi|10297535|dbj|AV695672.1|AV695672 AV695672 GKC Homo sapie... 989 0.0
gi|10289123|dbj|AV687260.1|AV687260 AV687260 GKC Homo sapie... 989 0.0
gi|13572512|gb|BG564859.1|BG564859 602589807F1 NIH_MGC_76 H... 977 0.0
gi|10301035|dbj|AV699064.1|AV699064 AV699064 GKC Homo sapie... 959 0.0
gi|5436727|gb|AI817648.1|AI817648 td15a06.x1 NCI_CGAP_Co16 ... 950 0.0
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gi|3734912|gb|AI184274.1|AI184274 qc63f10.x1 Soares_placent... 942 0.0
gi|3601482|gb|AI131466.1|AI131466 qc09c01.x1 Soares_fetal_h... 936 0.0
gi|1137815|gb|N23665.1|N23665 yw40b12.s1 Weizmann Olfactory... 910 0.0
gi|4223511|gb|AI393964.1|AI393964 tg11d10.x1 NCI_CGAP_CLL1 ... 906 0.0
gi|10297172|dbj|AV695309.1|AV695309 AV695309 GKC Homo sapie... 898 0.0
gi|10822421|gb|BF063511.1|BF063511 7h81e04.x1 NCI_CGAP_Co16... 860 0.0
gi|11107323|gb|BF213737.1|BF213737 601847627F1 NIH_MGC_55 H... 858 0.0
gi|11107339|gb|BF213753.1|BF213753 601847652F1 NIH_MGC_55 H... 852 0.0
gi|10289096|dbj|AV687233.1|AV687233 AV687233 GKC Homo sapie... 848 0.0
gi|6039642|gb|AW084490.1|AW084490 wz24e10.x1 Soares_Dieckgr... 837 0.0
gi|9881634|dbj|AV660620.1|AV660620 AV660620 GLC Homo sapien... 829 0.0
gi|9719903|gb|BE512784.1|BE512784 601171544F1 NIH_MGC_15 Ho... 823 0.0
gi|10297603|dbj|AV695740.1|AV695740 AV695740 GKC Homo sapie... 813 0.0
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>gi|4557649|ref|NP_000188.1| estradiol 17 beta-dehydrogenase 3; 17-beta-HSD3
[Homo sapiens]

EST Search:

N62871 multiple sclerosis lesion

N77777 multiple sclerosis lesion

Sequences producing significant alignments:	(bits)	Value
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gi|3429912|gb|AI090853.1|AI090853 ov44f05.x1 Soares_testis_... 1380 0.0
gi|2154248|gb|AA442370.1|AA442370 zv62c08.r1 Soares_testis_... 1053 0.0
gi|2154226|gb|AA442348.1|AA442348 zv62a08.r1 Soares_testis_... 1043 0.0
gi|2142185|gb|AA437271.1|AA437271 zv62a08.s1 Soares_testis_... 1017 0.0

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gi|2142205|gb|AA437291.1|AA437291 zv62c08.s1 Soares_testis_... 1003 0.0
gi|1210700|gb|N62871.1|N62871 yz83e04.s1 Soares_multiple_sc... 797 0.0
gi|1783826|gb|AA194135.1|AA194135 zr37f08.r1 Soares_NhHMPu_... 769 0.0
gi|6073356|gb|AW102743.1|AW102743 xd70e10.x1 SoaresNFL_T_G... 718 0.0
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gi|2993224|gb|AA883694.1|AA883694 al58b05.s1 SoaresNFL_T_G... 626 e-
177
gi|2837959|gb|AA778628.1|AA778628 af87b08.s1 Soares_testis_... 517 e-
144
gi|5446033|gb|AI825362.1|AI825362 wb17e09.x1 NCI_CGAP_GC6 H... 507 e-
141
gi|4682494|gb|AI631164.1|AI631164 ts93d10.x1 NCI_CGAP_GC6 H... 500 e-
139
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>gi|1706396|sp|P51659|DHB4_HUMAN ESTRADIOL 17 BETA-DEHYDROGENASE 4 (17-BETA-HSD 4) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4)

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi|12795330|emb|AL531837.1|AL531837 AL531837 LTNFL001_NBC... 1659 0.0
gi|13908294|gb|BG676897.1|BG676897 602623506F1 NCI_CGAP_Skn... 1631 0.0
gi|12914346|emb|AL564189.1|AL564189 AL564189 LTNFL001_NBC... 1586 0.0
gi|12879740|emb|AL546532.1|AL546532 AL546532 LTNFL006_PL2... 1524 0.0
gi|10949847|dbj|AU125131.1|AU125131 AU125131 NT2RM4 Homo sa... 1479 0.0
gi|10948684|dbj|AU123968.1|AU123968 AU123968 NT2RM2 Homo sa... 1479 0.0
gi|10992681|dbj|AU132327.1|AU132327 AU132327 NT2RP3 Homo sa... 1437 0.0
gi|3214525|gb|AI005015.1|AI005015 ou91a01.x1 NCI_CGAP_Kid3 ... 1427 0.0
gi|13721603|gb|BG199916.1|BG199916 RST19212 Athersys RAGE L... 1413 0.0
gi|3674126|gb|AI146444.1|AI146444 qb93a03.x1 Soares_fetal_h... 1402 0.0
gi|13911524|gb|BG680127.1|BG680127 602628285F1 NCI_CGAP_Skn... 1394 0.0
gi|3412550|gb|AI078142.1|AI078142 oz30b04.x1 Soares_total_f... 1394 0.0
gi|10991451|dbj|AU131097.1|AU131097 AU131097 NT2RP3 Homo sa... 1374 0.0
gi|5409861|emb|AL040917.1|AL040917 DKFZp434J2215_s1 434 (sy... 1372 0.0
gi|10795143|dbj|AV713626.1|AV713626 AV713626 DCB Homo sapie... 1348 0.0
gi|10991758|dbj|AU131404.1|AU131404 AU131404 NT2RP3 Homo sa... 1346 0.0
gi|10932266|dbj|AU117308.1|AU117308 AU117308 HEMBA1 Homo sa... 1346 0.0
gi|10996985|dbj|AU136446.1|AU136446 AU136446 PLACE1 Homo sa... 1344 0.0
gi|11004302|dbj|AU142781.1|AU142781 AU142781 Y79AA1 Homo sa... 1328 0.0
gi|10144826|gb|BE730834.1|BE730834 601569914F1 NIH_MGC_21 H... 1316 0.0
gi|9769065|gb|BE540420.1|BE540420 601065826F1 NIH_MGC_10 Ho... 1308 0.0
gi|12429277|gb|BG035291.1|BG035291 602324913F1 NIH_MGC_90 H... 1304 0.0
gi|10992834|dbj|AU132480.1|AU132480 AU132480 NT2RP3 Homo sa... 1292 0.0
gi|10365912|gb|BE898933.1|BE898933 601682360F1 NIH_MGC_9 Ho... 1292 0.0
gi|3002065|gb|AA886957.1|AA886957 oi14e10.s1 NCI_CGAP_GC4 H... 1291 0.0
gi|8169585|gb|AW978321.1|AW978321 EST390430 MAGE resequence... 1283 0.0
gi|10579372|gb|BE968667.1|BE968667 601650086F1 NIH_MGC_74 H... 1279 0.0
gi|10352702|gb|BE892403.1|BE892403 601433879F1 NIH_MGC_72 H... 1273 0.0
gi|14512082|gb|BI093752.1|BI093752 602860460F1 NIH_MGC_10 H... 1269 0.0
gi|6439061|gb|AW173113.1|AW173113 xj83d12.x1 SoaresNFL_T_G... 1247 0.0
gi|11264224|gb|BF315938.1|BF315938 601895882F1 NIH_MGC_19 H... 1231 0.0
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gi|10321137|gb|BE872361.1|BE872361 601448614F1 NIH_MGC_65 H... 1223 0.0
 gi|10355660|gb|BE893865.1|BE893865 601436228F1 NIH_MGC_72 H... 1221 0.0
 gi|10098245|gb|BE710071.1|BE710071 IL3-HT0618-030800-233-G0... 1217 0.0
 gi|11283822|gb|BF337571.1|BF337571 602035323F1 NCI_CGAP_Bm... 1191 0.0
 gi|10038238|gb|BE677697.1|BE677697 7d90e10.x1 Lupski_dorsal... 1187 0.0
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 gi|10725045|dbj|AV707780.1|AV707780 AV707780 ADB Homo sapie... 1178 0.0
 gi|12416699|gb|BG027664.1|BG027664 602294679F1 NIH_MGC_86 H... 1176 0.0
 gi|12101942|gb|BF796888.1|BF796888 602258274F1 NIH_MGC_85 H... 1174 0.0
 gi|1799096|gb|AA203386.1|AA203386 zx57f11.r1 Soares_fetal_I... 1170 0.0
 gi|13704200|gb|BG182513.1|BG182513 RST1389 Athersys RAGE Li... 1168 0.0
 gi|5393242|gb|AI806676.1|AI806676 wf35d04.x1 Soares_NFL_T_G... 1168 0.0
 gi|4875177|gb|AI674697.1|AI674697 wd19d06.x1 Soares_NFL_T_G... 1160 0.0
 gi|10965228|gb|BF126270.1|BF126270 601650451F1 NIH_MGC_76 H... 1154 0.0
 gi|6661159|gb|AW274129.1|AW274129 xv27b02.x1 Soares_NFL_T_G... 1148 0.0
 gi|5393220|gb|AI806654.1|AI806654 wf35b04.x1 Soares_NFL_T_G... 1144 0.0
 gi|13050584|gb|BG292110.1|BG292110 602386409F1 NIH_MGC_93 H... 1134 0.0
 gi|11968943|gb|BF683535.1|BF683535 602139737F1 NIH_MGC_46 H... 1128 0.0
 gi|12614085|gb|BG120576.1|BG120576 602346709F1 NIH_MGC_90 H... 1126 0.0
 gi|11978501|gb|BF693093.1|BF693093 602080115F1 NIH_MGC_81 H... 1126 0.0
 gi|10951089|dbj|AU126373.1|AU126373 AU126373 NT2RP1 Homo sa... 1122 0.0
 gi|10995386|dbj|AU134847.1|AU134847 AU134847 PLACE1 Homo sa... 1114 0.0
 gi|2992678|gb|AA883079.1|AA883079 am24a03.s1 Soares_NFL_T_G... 1114 0.0
 gi|10823746|dbj|AV721848.1|AV721848 AV721848 HTB Homo sapie... 1112 0.0
 gi|4893253|gb|AI683071.1|AI683071 tx01b04.x1 NCI_CGAP_Ut4 H... 1110 0.0
 gi|4610274|gb|AI601245.1|AI601245 ar88b08.x1 Barstead colon... 1098 0.0
 gi|10825009|dbj|AV722480.1|AV722480 AV722480 HTB Homo sapie... 1096 0.0
 gi|9132373|gb|BE312992.1|BE312992 601150276F1 NIH_MGC_19 Ho... 1094 0.0
 gi|13980573|gb|BG705833.1|BG705833 602669317F1 NIH_MGC_96 H... 1090 0.0
 gi|6451107|gb|AW182647.1|AW182647 xj45a04.x1 Soares_NFL_T_G... 1088 0.0
 gi|12674928|gb|BG168225.1|BG168225 602339543F1 NIH_MGC_89 H... 1082 0.0
 gi|12040732|gb|BF724821.1|BF724821 bx09b01.y1 Human Iris cD... 1082 0.0
 gi|10299269|dbj|AV697406.1|AV697406 AV697406 GKC Homo sapie... 1080 0.0
 gi|2185694|gb|AA460574.1|AA460574 zx60a12.r1 Soares_testis_... 1080 0.0
 gi|8149925|gb|AW960241.1|AW960241 EST372312 MAGE resequence... 1076 0.0
 gi|2261844|gb|AA521301.1|AA521301 aa79f07.s1 NCI_CGAP_GCB1 ... 1061 0.0
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 gi|6881860|gb|AW377197.1|AW377197 IL3-CT0220-111199-028-D09... 1041 0.0
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 gi|12916948|emb|AL565505.1|AL565505 AL565505 LTI_FL013_FBrn... 1031 0.0
 gi|10990261|dbj|AU129907.1|AU129907 AU129907 NT2RP2 Homo sa... 1031 0.0
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 gi|10203989|gb|BE782791.1|BE782791 601471972F1 NIH_MGC_67 H... 1015 0.0
 gi|9871380|dbj|AV650366.1|AV650366 AV650366 GLC Homo sapien... 1011 0.0
 gi|1961448|gb|AA309123.1|AA309123 EST179897 Colon carcinoma... 1011 0.0
 gi|14403997|gb|BG999925.1|BG999925 MR1-HN0069-040101-015-g1... 999 0.0
 gi|5036667|gb|AI719411.1|AI719411 as64c11.x1 Barstead colon... 993 0.0
 gi|10299583|dbj|AV697720.1|AV697720 AV697720 GKC Homo sapie... 991 0.0
 gi|2335271|gb|AA563632.1|AA563632 ng47f08.s1 NCI_CGAP_Co3 H... 983 0.0
 gi|11263172|gb|BF314998.1|BF314998 601899017F1 NIH_MGC_19 H... 977 0.0
 gi|2933392|gb|AA845633.1|AA845633 ai90c08.s1 Soares_parathy... 969 0.0
 gi|14172393|gb|BG824806.1|BG824806 602725101F1 NIH_MGC_15 H... 963 0.0
 gi|6038150|gb|AW082998.1|AW082998 xb72d12.x1 Soares_NFL_T_G... 959 0.0
 gi|3844111|gb|AI248714.1|AI248714 qh72c04.x1 Soares_fetal_I... 959 0.0
 gi|11012858|dbj|AU151337.1|AU151337 AU151337 NT2RP2 Homo sa... 957 0.0
 gi|9877013|dbj|AV655999.1|AV655999 AV655999 GLC Homo sapien... 957 0.0

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gi|5449606|gb|AI828935.1|AI828935 wj37h08.x1 NCI_CGAP_Lu19 ... 952 0.0
gi|11015393|dbj|AU153872.1|AU153872 AU153872 NT2RP3 Homo sa... 948 0.0
gi|2838179|gb|AA778848.1|AA778848 zj42a03.s1 Soares_fetal_... 946 0.0
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gi|3742671|gb|AI191462.1|AI191462 qe32f11.s1 Soares_fetal_... 940 0.0
gi|3596240|gb|AI127726.1|AI127726 qc26h03.x1 Soares_pregnan... 940 0.0
gi|4270907|gb|AI424976.1|AI424976 tg38g11.x1 Soares_NFL_T_G... 936 0.0
gi|2704986|gb|AA701873.1|AA701873 zi56b08.s1 Soares_fetal_... 932 0.0
gi|4073260|gb|AI336333.1|AI336333 qt43f09.x1 Soares_fetal_... 924 0.0
gi|4073310|gb|AI336383.1|AI336383 qt51c08.x1 Soares_fetal_... 916 0.0
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>gi|7705421|ref|NP_057455.1| hydroxysteroid (17-beta) dehydrogenase 7; 17 beta-hydroxysteroid dehydrogenase type VII [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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AA381145 activated T cells

AA381143 activated T cells

Sequences producing significant alignments:	(bits)	Value
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gi|12795928|emb|AL532435.1|AL532435 AL532435 LTI_NFL001_NBC... 1871 0.0
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gi|12385016|gb|BF982204.1|BF982204 602306244F1 NIH_MGC_88 H... 1302 0.0
gi|12097882|gb|BF792897.1|BF792897 602253394F1 NIH_MGC_84 H... 1221 0.0
gi|13403023|gb|BG470748.1|BG470748 602511688F1 NIH_MGC_16 H... 1168 0.0
gi|2881531|gb|AA811920.1|AA811920 ob72e11.s1 NCI_CGAP_GCB1 ... 1051 0.0
gi|14169203|gb|BG821616.1|BG821616 602727619F1 NIH_MGC_15 H... 1027 0.0
gi|13721684|gb|BG199997.1|BG199997 RST19294 Athersys RAGE L... 993 0.0
gi|10737010|gb|BF029298.1|BF029298 601765528F1 NIH_MGC_53 H... 977 0.0
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gi|4334333|gb|AI472243.1|AI472243 tj86g08.x1 Soares_NSF_F8... 934 0.0
gi|11162286|gb|BF247157.1|BF247157 601857822F1 NIH_MGC_58 H... 906 0.0
gi|10989791|dbj|AU129437.1|AU129437 AU129437 NT2RP2 Homo sa... 890 0.0
gi|13703900|gb|BG182213.1|BG182213 RST1077 Athersys RAGE Li... 884 0.0
gi|10992118|dbj|AU131764.1|AU131764 AU131764 NT2RP3 Homo sa... 876 0.0
gi|10988921|dbj|AU128567.1|AU128567 AU128567 NT2RP2 Homo sa... 868 0.0
gi|11363939|gb|BF382636.1|BF382636 601816836F1 NIH_MGC_56 H... 848 0.0
gi|8144565|gb|AW954882.1|AW954882 EST366952 MAGE resequence... 835 0.0
gi|9128432|gb|BE257950.1|BE257950 601109786F1 NIH_MGC_16 Ho... 801 0.0
gi|1844803|gb|AA224260.1|AA224260 zr15a04.r1 Stratagene NT2... 799 0.0
gi|9128029|gb|BE257566.1|BE257566 601109643F1 NIH_MGC_16 Ho... 797 0.0
gi|928055|gb|R83178.1|R83178 yp87e11.r1 Soares fetal liver ... 791 0.0
gi|12270902|gb|BF880776.1|BF880776 QV3-ET0174-011200-513-f0... 765 0.0
gi|10921244|dbj|AV763396.1|AV763396 AV763396 MDS Homo sapie... 700 0.0
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>gi|12643402|sp|Q92506|DHB8_HUMAN ESTRADIOL 17 BETA-DEHYDROGENASE 8 (17-BETA-HSD 8) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 8) (KE6 PROTEIN) (KE-6)

EST Search :

N47726 multiple sclerosis lesion

N47727 multiple sclerosis lesion

N98941 multiple sclerosis lesion

Sequences producing significant alignments:	(bits)	Value
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gi 12897211 emb AL555459.1 AL555459	AL555459	LTI_NFL006	PL2...	1296	0.0
gi 10391209 gb BE901734.1 BE901734	601675345F1	NIH_MGC_21	H...	1237	0.0
gi 14805093 gb BI253554.1 BI253554	602973478F1	NIH_MGC_12	H...	1203	0.0
gi 14619885 gb BI159884.1 BI159884	602863711F1	NIH_MGC_42	H...	1197	0.0
gi 2703586 gb AA700623.1 AA700623	zI43a04.s1	Soares_fetal_I...	...	1156	0.0
gi 12897209 emb AL555458.1 AL555458	AL555458	LTI_NFL006	PL2...	1136	0.0
gi 5394035 gb AI807469.1 AI807469	wf48b08.x1	SoaresNFL_T_G...	...	1120	0.0
gi 5878587 gb AW025057.1 AW025057	wu93f03.x1	NCI_CGAP_Kid3	...	1104	0.0
gi 11613994 gb BF526631.1 BF526631	602070755F1	NCI_CGAP_Brn...	...	1102	0.0
gi 12345465 gb BF978250.1 BF978250	602148205F1	NIH_MGC_62	H...	1084	0.0
gi 5839154 gb AI992249.1 AI992249	ws41d10.x1	NCI_CGAP_Brn25...	...	1027	0.0
gi 12411526 gb BG025183.1 BG025183	602276160F1	NIH_MGC_85	H...	995	0.0
gi 3766024 gb AI207352.1 AI207352	qg26d10.x1	NCI_CGAP_Kid3	...	995	0.0
gi 4268048 gb AI422117.1 AI422117	tf40g03.x1	NCI_CGAP_Brn23...	...	954	0.0
gi 2568438 gb AA643220.1 AA643220	nr96h03.s1	NCI_CGAP_Pr25	...	948	0.0
gi 4110767 gb AI359146.1 AI359146	qy26b08.x1	NCI_CGAP_Brn23...	...	890	0.0
gi 5838543 gb AI991715.1 AI991715	wt48a04.x1	NCI_CGAP_Pan1	...	819	0.0
gi 2942259 gb AA854721.1 AA854721	aj76h02.s1	Soares_parathy...	...	765	0.0
gi 5397037 gb AI810471.1 AI810471	wb89a09.x1	NCI_CGAP_Pr28	...	757	0.0
gi 4190811 gb AI380946.1 AI380946	tg18c12.x1	NCI_CGAP CLL1	...	747	0.0
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140

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>gi|2558754|gb|AAC51812.1| amyloid beta-peptide binding protein [Homo sapiens]; similar 17-beta-hydroxysteroid dehydrogenase type 10

EST Search:

Sequences producing significant alignments:	(bits)	Value
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AI 672661 spleen

AI572890 lymphoma

Sequences producing significant alignments:	(bits)	Value
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EST Search:

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gi|9179583|gb|BE296026.1|BE296026 601175058F1 NIH_MGC_17 Ho... 1128 0.0
gi|9770617|gb|BE541972.1|BE541972 601064273F1 NIH_MGC_10 Ho... 1126 0.0
gi|6568025|gb|AW235636.1|AW235636 xn20g09.x1 NCI_CGAP_Kid11... 1126 0.0
gi|12612166|gb|BG118660.1|BG118660 602348226F1 NIH_MGC_90 H... 1124 0.0
gi|13282164|gb|BG388718.1|BG388718 602414406F1 NIH_MGC_92 H... 1108 0.0
gi|11952959|gb|BF679064.1|BF679064 602153322F1 NIH_MGC_83 H... 1094 0.0
gi|11954261|gb|BF680366.1|BF680366 602154150F1 NIH_MGC_83 H... 1092 0.0
gi|13336068|gb|BG429562.1|BG429562 602501238F1 NIH_MGC_75 H... 1076 0.0
gi|11613456|gb|BF526180.1|BF526180 602071089F1 NCI_CGAP_Brn... 1076 0.0
gi|1544739|gb|AA053804.1|AA053804 ze25e09.s1 Soares_fetal_h... 1076 0.0
gi|11954238|gb|BF680343.1|BF680343 602154124F1 NIH_MGC_83 H... 1070 0.0
gi|2154395|gb|AA442517.1|AA442517 zv68a01.r1 Soares_total_f... 1068 0.0
gi|13727617|gb|BG205930.1|BG205930 RST25365 Athersys RAGE L... 1067 0.0
gi|11947983|gb|BF674088.1|BF674088 602137489F1 NIH_MGC_83 H... 1059 0.0
gi|14178068|gb|BG830481.1|BG830481 602767043F1 NIH_MGC_42 H... 1057 0.0
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gi|11947422|gb|BF673610.1|BF673610 602136021F1 NIH_MGC_83 H... 1055 0.0
gi|9135943|gb|BE262703.1|BE262703 601146057F1 NIH_MGC_19 Ho... 1055 0.0
gi|12523600|gb|BG057848.1|BG057848 naf13d09.x1 Soares_NPBMC... 1051 0.0
gi|11107340|gb|BF213754.1|BF213754 601847654F1 NIH_MGC_55 H... 1051 0.0
gi|11947265|gb|BF673370.1|BF673370 602135837F1 NIH_MGC_83 H... 1047 0.0
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gi|9189288|gb|BE336903.1|BE336903 bb68f05.y1 NIH_MGC_9 Homo... 1043 0.0
gi|10348906|gb|BE890514.1|BE890514 601431585F1 NIH_MGC_72 H... 1037 0.0
gi|12158715|gb|BF820301.1|BF820301 CM0-RT0018-181100-706-e0... 1029 0.0
gi|2167857|gb|AA454188.1|AA454188 zx48a12.s1 Soares_testis_... 1029 0.0
gi|12062595|gb|BF735895.1|BF735895 QV1-KT0023-131100-480-b0... 1027 0.0
gi|12062768|gb|BF736094.1|BF736094 QV1-KT0023-131100-475-h0... 1025 0.0
gi|5080879|gb|AF063505.1|AF063505 AF063505 Homo sapiens lib... 1023 0.0
gi|6359496|gb|AI110631.1|AI110631 HA0057 Human fetal liver ... 1023 0.0
gi|14471624|gb|BI064110.1|BI064110 IL3-UT0119-170401-458-F0... 1021 0.0
gi|10587293|gb|BE973957.1|BE973957 601680275F1 NIH_MGC_83 H... 1021 0.0
gi|14565160|gb|BI114259.1|BI114259 602862449F1 NIH_MGC_17 H... 1017 0.0
gi|11947398|gb|BF673586.1|BF673586 602136287F1 NIH_MGC_83 H... 1017 0.0
gi|11948042|gb|BF674147.1|BF674147 602137658F1 NIH_MGC_83 H... 1009 0.0
gi|11948071|gb|BF674176.1|BF674176 602137695F1 NIH_MGC_83 H... 1007 0.0
gi|12062604|gb|BF735904.1|BF735904 QV1-KT0023-131100-480-h0... 1005 0.0
gi|2703194|gb|AA700231.1|AA700231 zj52f03.s1 Soares_fetal_l... 1003 0.0
gi|5663000|gb|AI927036.1|AI927036 wo87b07.x1 NCI_CGAP_Kid11... 997 0.0
gi|11949270|gb|BF675375.1|BF675375 602138336F1 NIH_MGC_83 H... 993 0.0
gi|11107263|gb|BF213677.1|BF213677 601847527F1 NIH_MGC_55 H... 993 0.0
gi|5839186|gb|AI992281.1|AI992281 ws41g11.x1 NCI_CGAP_Brn25... 991 0.0
gi|4897519|gb|AI686225.1|AI686225 tu40f05.x1 NCI_CGAP_Pr28 ... 991 0.0
gi|5364540|gb|AI799068.1|AI799068 we98b05.x1 SoaresNFL_T_G... 989 0.0
gi|14471659|gb|BI064132.1|BI064132 IL3-UT0119-170401-459-H0... 983 0.0
gi|5864305|gb|AW015548.1|AW015548 UI-H-BI0p-aau-e-01-0-UI.s... 983 0.0
gi|11943604|gb|BF669709.1|BF669709 602118259F1 NIH_MGC_56 H... 981 0.0
gi|12062547|gb|BF735964.1|BF735964 QV1-KT0023-111100-479-b0... 979 0.0
gi|2167856|gb|AA454187.1|AA454187 zx48a12.r1 Soares_testis_... 977 0.0
gi|9969904|gb|BE645593.1|BE645593 7e72g02.x1 NCI_CGAP_Pr28 ... 975 0.0
gi|7280592|gb|AW593334.1|AW593334 hg13d03.x1 SoaresNFL_T_G... 975 0.0
gi|11954107|gb|BF680212.1|BF680212 602154965F1 NIH_MGC_83 H... 971 0.0

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gi|13335825|gb|BG429319.1|BG429319 602494022F1 NIH_MGC_75 H... 967 0.0
 gi|10578047|gb|BE967342.1|BE967342 601649342F1 NIH_MGC_73 H... 967 0.0
 gi|1686108|gb|AA126515.1|AA126515 zn85c12.s1 Stratagene lun... 965 0.0
 gi|5913719|gb|AW051449.1|AW051449 wy95h11.x1 NCI_CGAP_Brn23... 961 0.0
 gi|9156141|gb|BE281127.1|BE281127 601157756F1 NIH_MGC_21 Ho... 959 0.0
 gi|2584691|gb|AA653039.1|AA653039 ns71e08.s1 NCI_CGAP_Pr2 H... 959 0.0
 gi|11449515|gb|BF437182.1|BF437182 7p67e11.x1 NCI_CGAP_Pr28... 957 0.0
 gi|7632890|gb|AW732557.1|AW732557 bb08c01.y1 NIH_MGC_14 Hom... 955 0.0
 gi|11107822|gb|BF214236.1|BF214236 601848414F1 NIH_MGC_55 H... 946 0.0
 gi|5632015|gb|AI912160.1|AI912160 wd71a09.x1 NCI_CGAP_Lu24 ... 938 0.0
 gi|9156661|gb|BE281638.1|BE281638 601155146F1 NIH_MGC_21 Ho... 934 0.0
 gi|5886621|gb|AW027865.1|AW027865 ws62b11.x1 NCI_CGAP_Brn23... 932 0.0
 gi|9186545|gb|BE302797.1|BE302797 ba69a06.y1 NIH_MGC_20 Hom... 928 0.0
 gi|8364368|gb|BE047315.1|BE047315 hq78g07.x1 NCI_CGAP_Ov41 ... 928 0.0
 gi|6361052|gb|AI174674.1|AI174674 HA2365 Human fetal liver ... 928 0.0
 gi|10367360|gb|BE855387.1|BE855387 7g13b06.x1 NCI_CGAP_Brn2... 922 0.0
 gi|13970318|gb|BG700707.1|BG700707 602682353F1 NIH_MGC_95 H... 916 0.0
 gi|1507636|gb|AA035790.1|AA035790 ze25e09.r1 Soares_fetal_h... 916 0.0
 gi|1679019|gb|AA121396.1|AA121396 zn77h06.s1 Stratagene NT2... 914 0.0
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 gi|11681877|gb|BF589553.1|BF589553 naa05g08.x1 NCI_CGAP_Pr2... 910 0.0
 gi|10887537|gb|BF105011.1|BF105011 601822785F1 NIH_MGC_75 H... 908 0.0
 gi|5767638|gb|AI970812.1|AI970812 wr20b02.x1 NCI_CGAP_Pr28 ... 906 0.0
 gi|11950417|gb|BF676522.1|BF676522 602084429F1 NIH_MGC_83 H... 904 0.0
 gi|11108871|gb|BF215285.1|BF215285 601846338F1 NIH_MGC_55 H... 900 0.0
 gi|1383082|gb|W72327.1|W72327 zd62b11.s1 Soares_fetal_heart... 900 0.0

>gi|7705907|ref|NP_057330.1| retinal short-chain dehydrogenase/reductase
 retSDR3 [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 10370049 gb BE856729.1 BE856729 7f66h09.x1 Soares_NSF_F8...	1183	0.0
gi 3180757 gb AA994212.1 AA994212 ou49b10.s1 NCI_CGAP_Br2 H...	1104	0.0
gi 12102027 gb BF796973.1 BF796973 602258193F1 NIH_MGC_85 H...	1055	0.0
gi 4334141 gb AI472051.1 AI472051 tj85e10.x1 Soares_NSF_F8...	1047	0.0
gi 5394770 gb AI808204.1 AI808204 wf93f01.x1 Soares_NSF_F8...	1045	0.0
gi 8156902 gb AW967066.1 AW967066 EST379140 MAGE resequence...	1023	0.0
gi 9706163 gb BE503755.1 BE503755 hz51b10.x1 NCI_CGAP_Lu24 ...	1013	0.0
gi 4971779 gb AI694439.1 AI694439 wd83g04.x1 NCI_CGAP_Lu24 ...	1005	0.0
gi 5110372 gb AI742084.1 AI742084 wg38g06.x1 Soares_NSF_F8...	957	0.0
gi 3214671 gb AI005161.1 AI005161 ou13c05.x1 SoaresNFL_T_G...	940	0.0
gi 1523029 gb AA044826.1 AA044826 zk72b09.s1 Soares_pregnant...	918	0.0
gi 3594921 gb AI126407.1 AI126407 qc55g09.x1 Soares_placent...	902	0.0
gi 10964840 gb BF125800.1 BF125800 601763002F1 NIH_MGC_20 H...	894	0.0
gi 4523233 gb AI564776.1 AI564776 tn37b01.x1 NCI_CGAP_Brn25...	882	0.0
gi 4189789 gb AI379936.1 AI379936 tc53c09.x1 Soares_NhHMPu...	872	0.0
gi 10718270 gb AV701940.1 AV701940 AV701940 ADB Homo sapie...	835	0.0
gi 10941621 gb BF112008.1 BF112008 7l37e08.x1 Soares_NSF_F8...	817	0.0
gi 6946828 gb AW418896.1 AW418896 ha15c03.x1 NCI_CGAP_Kid12...	817	0.0

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>gi|3372592|gb|AAC39922.1| sterol/retinol dehydrogenase [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 9882144 dbj AV661130.1 AV661130	AV661130 GLC Homo sapien...	928 0.0
gi 10297142 dbj AV695279.1 AV695279	AV695279 GKC Homo sapie...	611 e-172
gi 10290555 dbj AV688692.1 AV688692	AV688692 GKC Homo sapie...	595 e-167
gi 9868702 dbj AV647688.1 AV647688	AV647688 GLC Homo sapien...	543 e-152
gi 9868612 dbj AV647598.1 AV647598	AV647598 GLC Homo sapien...	543 e-152
gi 9868272 dbj AV647258.1 AV647258	AV647258 GLC Homo sapien...	543 e-152
gi 9868493 dbj AV647479.1 AV647479	AV647479 GLC Homo sapien...	504 e-140

Jurkat Tcells: AA312392

gb AA381769.1 AA381769	EST94887 Activated T-cells Homo sa...	36 9.9
gb AA381726.1 AA381726	EST94873 Activated T-cells Homo sa...	36 9.9
gb AA381649.1 AA381649	EST94823 Activated T-cells Homo sa...	36 9.9
gb AA381695.1 AA381695	EST94806 Activated T-cells Homo sa...	36 9.9
gb AA381691.1 AA381691	EST94801 Activated T-cells Homo sa...	36 9.9
gb AA381683.1 AA381683	EST94792 Activated T-cells Homo sa...	36 9.9
gb AA381621.1 AA381621	EST94733 Activated T-cells Homo sa...	36 9.9
gb AA381348.1 AA381348	EST94418 Activated T-cells Homo sa...	36 9.9

>gi|5031765|ref|NP_005516.1| hydroxysteroid (11-beta) dehydrogenase 1 [Homo sapiens]

EST Search :

N59147	multiple sclerosis lesion
N75182	multiple sclerosis lesion

Sequences producing significant alignments:	(bits)	Value
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gi 13906209 gb BG674813.1 BG674813	602620946F1 NCI_CGAP_Skn...	1685 0.0
gi 13905643 gb BG674247.1 BG674247	602620212F1 NCI_CGAP_Skn...	1635 0.0
gi 13961308 gb BG696304.1 BG696304	602659453F1 NCI_CGAP_Skn...	1614 0.0
gi 14052781 gb BG742128.1 BG742128	602634002F1 NCI_CGAP_Skn...	1564 0.0
gi 14052023 gb BG741370.1 BG741370	602631924F1 NCI_CGAP_Skn...	1562 0.0
gi 13966183 gb BG698667.1 BG698667	602703031F1 NCI_CGAP_Skn...	1469 0.0
gi 14051962 gb BG741309.1 BG741309	602634443F1 NCI_CGAP_Skn...	1437 0.0
gi 13543809 gb BG545364.1 BG545364	602572590F1 NIH_MGC_77 H...	1382 0.0

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gi|13964039|gb|BG697623.1|BG697623 602660865F1 NCI_CGAP_Skn... 1376 0.0
gi|13972710|gb|BG701903.1|BG701903 602683260F1 NIH_MGC_95 H... 1350 0.0
gi|13573357|gb|BG565704.1|BG565704 602589036F1 NIH_MGC_76 H... 1336 0.0
gi|9438885|gb|BE439403.1|BE439403 HTM1-018F1 HTM1 Homo sapi... 1255 0.0
gi|9872526|dbj|AV651512.1|AV651512 AV651512 GLC Homo sapien... 1223 0.0
gi|14053029|gb|BG742376.1|BG742376 602631760F1 NCI_CGAP_Skn... 1219 0.0
gi|11987203|gb|BF701795.1|BF701795 602129255F2 NIH_MGC_56 H... 1219 0.0
gi|13673667|gb|BG622296.1|BG622296 602646960F1 NIH_MGC_79 H... 1215 0.0
gi|13531288|gb|BG539055.1|BG539055 602568425F1 NIH_MGC_77 H... 1168 0.0
gi|10911141|dbj|AV753293.1|AV753293 AV753293 NPD Homo sapie... 1045 0.0
gi|12512467|gb|BG055093.1|BG055093 nac99e06.x1 NCI_CGAP_Pr2... 1039 0.0
gi|11984275|gb|BF698867.1|BF698867 602126436F1 NIH_MGC_56 H... 1021 0.0
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gi|14051178|gb|BG740525.1|BG740525 602633033F1 NCI_CGAP_Skn... 971 0.0
gi|9876959|dbj|AV655945.1|AV655945 AV655945 GLC Homo sapien... 957 0.0
gi|9872114|dbj|AV651100.1|AV651100 AV651100 GLC Homo sapien... 955 0.0
gi|9871963|dbj|AV650949.1|AV650949 AV650949 GLC Homo sapien... 955 0.0
gi|10291657|dbj|AV689794.1|AV689794 AV689794 GKC Homo sapie... 932 0.0
gi|9439140|gb|BE439658.1|BE439658 HTM1-325F HTM1 Homo sapie... 926 0.0
gi|3752813|gb|AI200207.1|AI200207 qf92a08.x1 Soares_placent... 902 0.0
gi|1679084|gb|AA121470.1|AA121470 zk91d05.r1 Soares_pregnant... 842 0.0
gi|1237760|gb|N75182.1|N75182_yz62g12.r1 Soares_multiple_sc... 827 0.0
gi|3645147|gb|AI139163.1|AI139163 qc23f09.x1 Soares_pregnant... 811 0.0

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>gi|14776198|ref|XP_043103.1| hydroxysteroid (11-beta) dehydrogenase 2
[Homo sapiens]

EST Search :

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gi 12883011 emb AL548215.1 AL548215 AL548215 LTI_NFL006_PL2...	1709	0.0
gi 12888948 emb AL551216.1 AL551216 AL551216 LTI_NFL006_PL2...	1673	0.0
gi 12935463 emb AL574858.1 AL574858 AL574858 LTI_NFL006_PL2...	1612	0.0
gi 12931533 emb AL572859.1 AL572859 AL572859 LTI_NFL006_PL2...	1610	0.0
gi 14506196 gb BI087866.1 BI087866 602852664F1 NIH_MGC_10 H...	1328	0.0
gi 12924205 emb AL569153.1 AL569153 AL569153 LTI_FL002_PL1 ...	1201	0.0
gi 12894985 emb AL554320.1 AL554320 AL554320 LTI_NFL006_PL2...	1197	0.0
gi 12444516 gb BG003850.1 BG003850 MR3-GN0187-201100-010-g0...	1138	0.0
gi 5111814 gb AI743526.1 AI743526 wf72c10.x2 Soares_NFL_T_G...	1126	0.0
gi 11767117 gb BE963698.2 BE963698 601657032R1 NIH_MGC_67 H...	1078	0.0
gi 2280229 gb AA535976.1 AA535976 nf95a05.s1 NCI_CGAP_Co3 H...	1017	0.0
gi 2278552 gb AA534299.1 AA534299 nf73d11.s1 NCI_CGAP_Co3 H...	1015	0.0
gi 12446016 gb BG004736.1 BG004736 MR3-GN0187-211100-009-f0...	1007	0.0
gi 12939828 emb AL577064.1 AL577064 AL577064 LTI_NFL006_PL2...	981	0.0
gi 3840588 gb AI245191.1 AI245191 qk22d10.x1 NCI_CGAP_Kid3 ...	963	0.0
gi 4111819 gb AI360198.1 AI360198 qy84a11.x1 NCI_CGAP_Brn25...	924	0.0
gi 3057842 gb AA917952.1 AA917952 ol68g12.s1 NCI_CGAP_Kid3 ...	918	0.0
gi 12441996 gb BG002650.1 BG002650 MR3-GN0187-171100-003-c0...	910	0.0
gi 4329685 gb AI476640.1 AI476640 tm23a04.x1 Soares_NFL_T_G...	890	0.0
gi 12758118 gb BG248303.1 BG248303 602400339F1 NIH_MGC_15 H...	878	0.0
gi 1776122 gb AA189088.1 AA189088 zq45c08.s1 Stratagene hNT...	874	0.0
gi 12393991 gb BF987669.1 BF987669 QV0-GN0141-121000-433-a0...	866	0.0
gi 5128365 gb AI750101.1 AI750101 at35h04.x1 Barstead colon...	866	0.0
gi 3801491 gb AI219288.1 AI219288 qg18c11.x1 Soares_placent...	823	0.0
gi 14253306 gb BG876216.1 BG876216 QV4-CT0361-140200-101-a0...	819	0.0
gi 13139762 gb BG333324.1 BG333324 602431361F1 NIH_MGC_18 H...	817	0.0
gi 3679683 gb AI151214.1 AI151214 qc73h09.x1 Soares_placent...	811	0.0
gi 3741199 gb AI189990.1 AI189990 qd25a10.x1 Soares_placent...	803	0.0
gi 12401269 gb BF994842.1 BF994842 QV0-GN0211-031100-471-a0...	795	0.0
gi 12162695 gb BF822586.1 BF822586 CM2-RT0009-071200-604-a0...	793	0.0
gi 3595626 gb AI127112.1 AI127112 qb98a09.x1 Soares_fetal_h...	793	0.0
gi 10893038 gb BF087328.1 BF087328 QV2-HT0540-120900-356-b0...	787	0.0
gi 3307586 gb AI050781.1 AI050781 ov12a05.x1 NCI_CGAP_Kid3 ...	787	0.0
gi 12370277 gb BF953002.1 BF953002 QV3-NN0198-111100-373-f0...	765	0.0
gi 7956033 gb AW860340.1 AW860340 RC0-CT0380-210300-035-g09...	757	0.0
gi 14385887 gb BG983048.1 BG983048 IL5-CN0068-060301-381-d0...	749	0.0
gi 4568562 gb AI582665.1 AI582665 tn16b05.x1 NCI_CGAP_Brn25...	737	0.0
gi 4567538 gb AI581641.1 AI581641 as03f05.x1 Barstead colon...	726	0.0
gi 2694936 gb AA693998.1 AA693998 zi48b09.s1 Soares_fetal_l...	724	0.0
gi 856647 gb R80366.1 R80366 yi96g01.r1 Soares_placenta Nb2...	724	0.0
gi 2716774 gb AA706856.1 AA706856 zi21c10.s1 Soares_fetal_l...	720	0.0

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>gi|4504479|ref|NP_000851.1| hydroxyprostaglandin dehydrogenase 15-(NAD)
[Homo sapiens]

EST Search:

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gi 12873492 emb AL541940.1 AL541940	AL541940 LTI_FL002_PL1 ...	1877 0.0
gi 12875081 emb AL542740.1 AL542740	AL542740 LTI_FL002_PL1 ...	1855 0.0
gi 10932989 dbj AU117975.1 AU117975	AU117975 HEMBA1 Homo sa...	1419 0.0
gi 10995644 dbj AU135105.1 AU135105	AU135105 PLACE1 Homo sa...	1415 0.0
gi 10996543 dbj AU136004.1 AU136004	AU136004 PLACE1 Homo sa...	1409 0.0
gi 13040302 gb BG286949.1 BG286949	602382834F1 NIH_MGC_93 H...	1400 0.0
gi 11001299 dbj AU139778.1 AU139778	AU139778 PLACE1 Homo sa...	1388 0.0
gi 10997253 dbj AU136714.1 AU136714	AU136714 PLACE1 Homo sa...	1382 0.0
gi 13669926 gb BG618555.1 BG618555	602645464F2 NIH_MGC_76 H...	1364 0.0
gi 13578224 gb BG570571.1 BG570571	602591255F1 NIH_MGC_77 H...	1354 0.0
gi 10996695 dbj AU136156.1 AU136156	AU136156 PLACE1 Homo sa...	1354 0.0
gi 10995511 dbj AU134972.1 AU134972	AU134972 PLACE1 Homo sa...	1354 0.0
gi 10997831 dbj AU137292.1 AU137292	AU137292 PLACE1 Homo sa...	1352 0.0
gi 13039192 gb BG286372.1 BG286372	602383144F1 NIH_MGC_93 H...	1350 0.0
gi 13048908 gb BG291198.1 BG291198	602388639F1 NIH_MGC_93 H...	1344 0.0
gi 13546833 gb BG548168.1 BG548168	602575324F1 NIH_MGC_77 H...	1342 0.0
gi 10999798 dbj AU138277.1 AU138277	AU138277 PLACE1 Homo sa...	1340 0.0
gi 14048877 gb BG778560.1 BG778560	602668005F1 NIH_MGC_60 H...	1338 0.0
gi 13574910 gb BG567257.1 BG567257	602589738F1 NIH_MGC_76 H...	1330 0.0
gi 13715496 gb BG193809.1 BG193809	RST12945 Athersys RAGE L...	1330 0.0
gi 12924251 emb AL569176.1 AL569176	AL569176 LTI_FL002_PL1 ...	1328 0.0
gi 10998094 dbj AU137555.1 AU137555	AU137555 PLACE1 Homo sa...	1320 0.0
gi 13572596 gb BG564943.1 BG564943	602583911F1 NIH_MGC_76 H...	1310 0.0
gi 13528136 gb BG536590.1 BG536590	602566204F1 NIH_MGC_77 H...	1298 0.0
gi 13044260 gb BG288929.1 BG288929	602383878F1 NIH_MGC_93 H...	1296 0.0
gi 11000464 dbj AU138943.1 AU138943	AU138943 PLACE1 Homo sa...	1292 0.0
gi 10997016 dbj AU136477.1 AU136477	AU136477 PLACE1 Homo sa...	1289 0.0
gi 10151099 gb BE737107.1 BE737107	601304459F1 NIH_MGC_39 H...	1281 0.0
gi 11000653 dbj AU139132.1 AU139132	AU139132 PLACE1 Homo sa...	1279 0.0
gi 13039746 gb BG286666.1 BG286666	602381684F1 NIH_MGC_93 H...	1267 0.0
gi 10932798 dbj AU117801.1 AU117801	AU117801 HEMBA1 Homo sa...	1261 0.0
gi 10995272 dbj AU134733.1 AU134733	AU134733 PLACE1 Homo sa...	1253 0.0
gi 13049252 gb BG291389.1 BG291389	602387263F1 NIH_MGC_93 H...	1235 0.0
gi 13045000 gb BG289298.1 BG289298	602387415F1 NIH_MGC_93 H...	1233 0.0
gi 11001529 dbj AU140008.1 AU140008	AU140008 PLACE1 Homo sa...	1231 0.0
gi 13044292 gb BG288945.1 BG288945	602383896F1 NIH_MGC_93 H...	1223 0.0
gi 10997197 dbj AU136658.1 AU136658	AU136658 PLACE1 Homo sa...	1221 0.0
gi 10996351 dbj AU135812.1 AU135812	AU135812 PLACE1 Homo sa...	1219 0.0
gi 14050602 gb BG739949.1 BG739949	602630904F1 NCI_CGAP_Skn...	1213 0.0
gi 13521654 gb BG530117.1 BG530117	602558603F1 NIH_MGC_61 H...	1211 0.0
gi 13294287 gb BG400839.1 BG400839	602464062F1 NIH_MGC_75 H...	1193 0.0
gi 10996117 dbj AU135578.1 AU135578	AU135578 PLACE1 Homo sa...	1187 0.0
gi 10995111 dbj AU134572.1 AU134572	AU134572 PLACE1 Homo sa...	1187 0.0
gi 13416849 gb BG484570.1 BG484570	602505736F1 NIH_MGC_77 H...	1185 0.0
gi 13342897 gb BG436391.1 BG436391	602509051F1 NIH_MGC_79 H...	1183 0.0
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gi 13340956 gb BG434450.1 BG434450	602506473F1 NIH_MGC_79 H...	1156 0.0
gi 13342591 gb BG436085.1 BG436085	602508877F1 NIH_MGC_79 H...	1154 0.0

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gi|13416352|gb|BG484073.1|BG484073 602504677F1 NIH_MGC_77 H... 1146 0.0
gi|12938589|emb|AL576441.1|AL576441 AL576441 LTI_NFL006_PL2... 1146 0.0
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gi|13041924|gb|BG287765.1|BG287765 602384115F1 NIH_MGC_93 H... 1134 0.0
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gi|10141065|gb|BE727073.1|BE727073 601563751F1 NIH_MGC_20 H... 1120 0.0
gi|13673902|gb|BG622531.1|BG622531 602647264F1 NIH_MGC_79 H... 1118 0.0
gi|9325374|gb|BE380009.1|BE380009 601159319F2 NIH_MGC_53 Ho... 1118 0.0
gi|10995892|dbj|AU135353.1|AU135353 AU135353 PLACE1 Homo sa... 1094 0.0
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gi|13341323|gb|BG434817.1|BG434817 602507341F1 NIH_MGC_79 H... 1084 0.0
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gi|11081229|gb|BF194909.1|BF194909 7a90b11.x1 NCI_CGAP_Kid1... 1061 0.0
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gi|13712893|gb|BG191206.1|BG191206 RST10293 Athersys RAGE L... 1023 0.0
gi|11001465|dbj|AU139944.1|AU139944 AU139944 PLACE1 Homo sa... 1021 0.0
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gi|10315127|gb|BE866442.1|BE866442 601678681F1 NIH_MGC_53 H... 997 0.0
gi|11017265|dbj|AU155744.1|AU155744 AU155744 PLACE1 Homo sa... 991 0.0
gi|10997723|dbj|AU137184.1|AU137184 AU137184 PLACE1 Homo sa... 987 0.0
gi|13342905|gb|BG436399.1|BG436399 602509061F1 NIH_MGC_79 H... 965 0.0
gi|10735967|gb|BF028255.1|BF028255 601765033F1 NIH_MGC_53 H... 957 0.0
gi|13673548|gb|BG622177.1|BG622177 602646815F1 NIH_MGC_79 H... 954 0.0
gi|6576242|gb|AW242488.1|AW242488 xm99e10.x1 NCI_CGAP_Kid11... 948 0.0
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gi|11155126|gb|BF241201.1|BF241201 601880081F1 NIH_MGC_55 H... 940 0.0
gi|2834557|gb|AA775223.1|AA775223 ac79e08.s1 Stratagene lun... 940 0.0
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gi|3888220|gb|AI269053.1|AI269053 qi24f07.x1 Soares_NhHMPu... 930 0.0
gi|12041908|gb|BF725997.1|BF725997 bx22g02.y1 Human Iris cD... 926 0.0
gi|10996590|dbj|AU136051.1|AU136051 AU136051 PLACE1 Homo sa... 920 0.0
gi|10735132|gb|BF027420.1|BF027420 601672490F1 NIH_MGC_20 H... 920 0.0
gi|11000958|dbj|AU139437.1|AU139437 AU139437 PLACE1 Homo sa... 916 0.0
gi|10584213|gb|BE971156.1|BE971156 601651108F1 NIH_MGC_81 H... 914 0.0

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>gi|7705925|ref|NP_057370.1| carbonyl reductase [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 14177680 gb BG830093.1 BG830093	602764845F1 NIH_MGC_42 H...	1491 0.0
gi 13404430 gb BG472244.1 BG472244	602513756F1 NIH_MGC_16 H...	1443 0.0
gi 14568476 gb BI117575.1 BI117575	602866754F1 NIH_MGC_7 Ho...	1419 0.0
gi 13982131 gb BG706614.1 BG706614	602674104F1 NIH_MGC_96 H...	1380 0.0
gi 13976241 gb BG703674.1 BG703674	602686647F1 NIH_MGC_95 H...	1368 0.0
gi 10390490 gb BE901372.1 BE901372	601674675F1 NIH_MGC_21 H...	1354 0.0
gi 12343809 gb BF976594.1 BF976594	602244271F1 NIH_MGC_48 H...	1326 0.0
gi 11641972 gb BF568592.1 BF568592	602184218F1 NIH_MGC_42 H...	1326 0.0
gi 11970704 gb BF685296.1 BF685296	602141648F1 NIH_MGC_46 H...	1304 0.0
gi 11252161 gb BF305282.1 BF305282	601892747F1 NIH_MGC_17 H...	1304 0.0
gi 11098442 gb BF204856.1 BF204856	601867158F1 NIH_MGC_17 H...	1300 0.0
gi 9137251 gb BE263706.1 BE263706	601192146F1 NIH_MGC_7 Hom...	1279 0.0
gi 10404479 gb BE909167.1 BE909167	601501782F1 NIH_MGC_70 H...	1277 0.0
gi 11151599 gb BF237681.1 BF237681	601841865F1 NIH_MGC_46 H...	1275 0.0
gi 9156256 gb BE281240.1 BE281240	601155341F1 NIH_MGC_21 Ho...	1275 0.0
gi 12342418 gb BF975203.1 BF975203	602244705F1 NIH_MGC_48 H...	1269 0.0
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gi 12683322 gb BG176619.1 BG176619	602313206F1 NIH_MGC_85 H...	1235 0.0
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gi 1148734 gb N30214.1 N30214	yw83h09.s1 Soares_placenta_8t...	1017 0.0
gi 13137575 gb BG331137.1 BG331137	602431839F1 NIH_MGC_18 H...	1013 0.0

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gi|9866354|dbj|AV645340.1|AV645340 AV645340 GLA Homo sapien... 1011 0.0
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 gi|4598919|gb|AI589871.1|AI589871 tm81d01.x1 NCI_CGAP_Brn25... 823 0.0
 gi|4489893|gb|AI557530.1|AI557530 pt2.1-06.D05b.r tumor2 Ho... 823 0.0
 gi|9874547|dbj|AV653533.1|AV653533 AV653533 GLC Homo sapien... 803 0.0
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>gi|4503817|ref|NP_002026.1| follicular lymphoma variant translocation 1
 [Homo sapiens]

EST Search:

Sequences producing significant alignments: (bits) Value

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 gi|10994408|dbj|AU133869.1|AU133869 AU133869 OVARC1 Homo sa... 1316 0.0
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gi|13049086|gb|BG291280.1|BG291280 602388439F1 NIH_MGC_93 H... 1265 0.0
gi|13289457|gb|BG396009.1|BG396009 602458738F1 NIH_MGC_16 H... 1223 0.0
gi|13999988|gb|BG720801.1|BG720801 602692025F1 NIH_MGC_97 H... 1203 0.0
gi|10293319|dbj|AV691456.1|AV691456 AV691456 GKC Homo sapien... 1130 0.0
gi|10936667|dbj|AU121432.1|AU121432 AU121432 MAMMA1 Homo sapien... 1126 0.0
gi|14511044|gb|BI092714.1|BI092714 602858508F1 NIH_MGC_10 H... 1090 0.0
gi|13526132|gb|BG534590.1|BG534590 602553441F1 NIH_MGC_77 H... 1090 0.0
gi|10995473|dbj|AU134934.1|AU134934 AU134934 PLACE1 Homo sapien... 1045 0.0
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gi|9185496|gb|BE301748.1|BE301748 bb77h08.x1 NIH_MGC_12 Hom... 876 0.0
gi|5397891|gb|AI811325.1|AI811325 tw38d08.x1 NCI_CGAP_Ut1 H... 876 0.0
gi|4176027|gb|AI376037.1|AI376037 ta57h08.x1 Soares_total_f... 876 0.0
gi|2933339|gb|AA845580.1|AA845580 ak04f02.s1 Soares_parathy... 876 0.0
gi|5132786|gb|AI754522.1|AI754522 cr26d08.x1 Jia bone marro... 870 0.0
gi|4113305|gb|AI361684.1|AI361684 qy90h03.x1 NCI_CGAP_Brn25... 868 0.0
gi|3959459|gb|AI300113.1|AI300113 qn59h09.x1 NCI_CGAP_Kid5 ... 868 0.0
gi|3601540|gb|AI131524.1|AI131524 qc13h09.x1 Soares_fetal_h... 868 0.0
gi|2336669|gb|AA565030.1|AA565030 nj11g07.s1 NCI_CGAP_Pr22 ... 868 0.0
gi|2265380|gb|AA524452.1|AA524452 ng45b01.s1 NCI_CGAP_Co3 H... 868 0.0
gi|12336897|gb|BF969682.1|BF969682 602272067F1 NIH_MGC_84 H... 862 0.0
gi|3596148|gb|AI127634.1|AI127634 qc30f11.x1 Soares_pregnant... 862 0.0
gi|4264050|gb|AI418119.1|AI418119 tf73h07.x1 NCI_CGAP_Brn23... 860 0.0
gi|3934574|gb|AI291800.1|AI291800 qm75d07.x1 Soares_placent... 860 0.0
gi|5133017|gb|AI754753.1|AI754753 cr29f09.x1 Jia bone marro... 858 0.0
gi|1157254|gb|N36112.1|N36112 yy32f04.s1 Soares_melanocyte ... 854 0.0
gi|6200565|gb|AW152665.1|AW152665 xf77g03.x1 NCI_CGAP_Gas4 ... 852 0.0
gi|3110443|gb|AA947048.1|AA947048 oq57d09.s1 NCI_CGAP_Kid6 ... 852 0.0
gi|11008839|dbj|AU147318.1|AU147318 AU147318 MAMMA1 Homo sapien... 850 0.0
gi|5854880|gb|AW006102.1|AW006102 wz92d03.x1 NCI_CGAP_Brn25... 850 0.0
gi|6463721|gb|AW189265.1|AW189265 xl03f02.x1 NCI_CGAP_Ut4 H... 848 0.0
gi|9873394|dbj|AV652380.1|AV652380 AV652380 GLC Homo sapien... 842 0.0
gi|1219078|gb|N66953.1|N66953 za48g10.s1 Soares_fetal_liver... 842 0.0
gi|3844217|gb|AI248820.1|AI248820 qh72e03.x1 Soares_fetal_l... 829 0.0
gi|7038930|gb|AW468824.1|AW468824 hd28f02.x1 Soares_NFL_T_G... 821 0.0
gi|3752125|gb|AI199519.1|AI199519 qj56h10.x1 NCI_CGAP_Brn25... 819 0.0
gi|11017247|dbj|AU155726.1|AU155726 AU155726 PLACE1 Homo sapien... 817 0.0
gi|10314879|gb|BE866103.1|BE866103 601679103F1 NIH_MGC_53 H... 817 0.0
gi|1350226|gb|W52783.1|W52783 zd13h07.r1 Soares_fetal_heart... 813 0.0
gi|3429339|gb|AI090280.1|AI090280 qb28f11.x1 Soares_pregnant... 809 0.0
gi|1156184|gb|N35042.1|N35042 yy17e01.s1 Soares_melanocyte ... 807 0.0
gi|4153051|gb|AI373185.1|AI373185 qz13e06.x1 NCI_CGAP CLL1 ... 803 0.0

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>gi|4503891|ref|NP_000394.1| UDP-galactose-4-epimerase; UDP galactose-4-epimerase; galactowaldenase [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 12899882 emb AL556844.1 AL556844	AL556844	LTI_NFL006_PL2...	1739	0.0
gi 12943580 emb AL578982.1 AL578982	AL578982	LTI_NFL006_PL2...	1699	0.0
gi 12791395 emb AL527902.1 AL527902	AL527902	LTI_NFL003_NBC...	1657	0.0
gi 12935014 emb AL574629.1 AL574629	AL574629	LTI_NFL006_PL2...	1643	0.0
gi 12884919 emb AL549184.1 AL549184	AL549184	LTI_NFL006_PL2...	1570	0.0
gi 12800245 emb AL536752.1 AL536752	AL536752	LTI_FL013_FBr...	1554	0.0
gi 13582317 gb BG574664.1 BG574664	602596666F1	NIH_MGC_87 H...	1475	0.0
gi 13401772 gb BG469497.1 BG469497	602532809F1	NIH_MGC_15 H...	1457	0.0
gi 13909656 gb BG678259.1 BG678259	602624574F1	NCI_CGAP_Skn...	1443	0.0
gi 12759023 gb BG249207.1 BG249207	602361637F1	NIH_MGC_89 H...	1404	0.0
gi 12787709 emb AL524216.1 AL524216	AL524216	LTI_NFL003_NBC...	1394	0.0
gi 10146723 gb BE732731.1 BE732731	601565201F1	NIH_MGC_21 H...	1386	0.0
gi 12918864 emb AL566474.1 AL566474	AL566474	LTI_FL013_FBr...	1380	0.0
gi 10141023 gb BE727031.1 BE727031	601563701F1	NIH_MGC_20 H...	1378	0.0
gi 12419290 gb BG030193.1 BG030193	602297382F1	NIH_MGC_87 H...	1372	0.0
gi 12601828 gb BG107982.1 BG107982	602278281F1	NIH_MGC_86 H...	1370	0.0
gi 12793968 emb AL530475.1 AL530475	AL530475	LTI_NFL001_NBC...	1362	0.0
gi 12426779 gb BG033962.1 BG033962	602301070F1	NIH_MGC_87 H...	1330	0.0
gi 13144832 gb BG338394.1 BG338394	602436183F1	NIH_MGC_46 H...	1324	0.0
gi 14505450 gb BI087120.1 BI087120	602850790F1	NIH_MGC_10 H...	1306	0.0
gi 13461976 gb BG500459.1 BG500459	602544981F1	NIH_MGC_60 H...	1304	0.0
gi 13140715 gb BG334277.1 BG334277	602461781F1	NIH_MGC_20 H...	1298	0.0
gi 3087051 gb AA932009.1 AA932009	om84a11.s1	NCI_CGAP_Kid3 ...	1287	0.0
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gi 13328160 gb BG421654.1 BG421654	602449748F1	NIH_MGC_14 H...	1277	0.0
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gi 12913462 emb AL563756.1 AL563756	AL563756	LTI_NFL001_NBC...	1247	0.0
gi 12788023 emb AL524530.1 AL524530	AL524530	LTI_NFL003_NBC...	1241	0.0
gi 14061340 gb BG750674.1 BG750674	602708562F1	NIH_MGC_43 H...	1223	0.0
gi 2823895 gb AA772112.1 AA772112	ai40b11.s1	Soares_parathy...	1203	0.0
gi 12932776 emb AL573485.1 AL573485	AL573485	LTI_NFL006_PL2...	1201	0.0
gi 3959421 gb AI300075.1 AI300075	qn59e05.x1	NCI_CGAP_Kid5 ...	1183	0.0
gi 14507383 gb BI089053.1 BI089053	602853414F1	NIH_MGC_10 H...	1178	0.0
gi 11098747 gb BF205161.1 BF205161	601866902F1	NIH_MGC_17 H...	1174	0.0
gi 4764219 gb AI660636.1 AI660636	wf23a09.x1	Soares_Dieckgr...	1166	0.0
gi 14071426 gb BG760786.1 BG760786	602717144F1	NIH_MGC_49 H...	1162	0.0
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gi 2348271 gb AA573756.1 AA573756	nk07c02.s1	NCI_CGAP_Co2 H...	1124	0.0
gi 2409414 gb AA594064.1 AA594064	nn16g10.s1	NCI_CGAP_Co12 ...	1088	0.0
gi 9334109 gb BE388744.1 BE388744	601283824F1	NIH_MGC_44 Ho...	1084	0.0
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gi 11253252 gb BF306167.1 BF306167	601893016F1	NIH_MGC_17 H...	1059	0.0
gi 11107300 gb BF213714.1 BF213714	601847578F1	NIH_MGC_55 H...	1053	0.0
gi 9331897 gb BE386532.1 BE386532	601273783F1	NIH_MGC_20 Ho...	1051	0.0
gi 6037026 gb AW081874.1 AW081874	xb56d11.x1	NCI_CGAP_Eso2 ...	1051	0.0
gi 5765666 gb AI968848.1 AI968848	wt93g02.x1	NCI_CGAP_GC6 H...	1037	0.0

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gi|13038030|gb|BG285754.1|BG285754 602380818F1 NIH_MGC_93 H... 1035 0.0
gi|12791394|emb|AL527901.1|AL527901 AL527901 LTI_NFL003_NBC... 1023 0.0
gi|9888038|gb|BE617100.1|BE617100 601441635F1 NIH_MGC_65 Ho... 1013 0.0
gi|4618533|gb|AI609366.1|AI609366 tw30g01.x1 NCI_CGAP_Ov35 ... 1007 0.0
gi|9330183|gb|BE384818.1|BE384818 601276175F1 NIH_MGC_20 Ho... 995 0.0
gi|6131515|gb|AW129910.1|AW129910 xf25a03.x1 NCI_CGAP_Kid8 ... 993 0.0
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gi|5436394|gb|AI817315.1|AI817315 wk36f10.x1 NCI_CGAP_Pr22 ... 977 0.0
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gi|12788022|emb|AL524529.1|AL524529 AL524529 LTI_NFL003_NBC... 969 0.0
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gi|4137868|gb|AI368123.1|AI368123 qq44e05.x1 Soares_total_f... 930 0.0
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gi|1687010|gb|AA127721.1|AA127721 zk92b07.s1 Soares_pregnant... 900 0.0
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gi|5512301|gb|AI858685.1|AI858685 wl41a12.x1 NCI_CGAP_Ut1 H... 898 0.0
gi|3841337|gb|AI245940.1|AI245940 qk45a03.x1 NCI_CGAP_Co8 H... 894 0.0
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gi|1801454|gb|AA206021.1|AA206021 zq54d10.s1 Stratagene neu... 884 0.0
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gi|1371254|gb|W63673.1|W63673 zd30a04.s1 Soares_fetal_heart... 882 0.0
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gi|1977901|gb|AA325658.1|AA325658 EST28681 Cerebellum II Ho... 801 0.0

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>gi|7705791|ref|NP_057110.1| CGI-82 protein [Homo sapiens]
Prostate short-chain dehydrogenase reductase 1

EST Search:

Organ: colon
Tissue type: adenocarcinoma cell line

Organ: skin

Organ: brain
Tissue type: hippocampus

Organ: skin
Tissue type: melanotic melanoma

Organ: ovary
Tissue type: adenocarcinoma cell line

Sequences producing significant alignments:	(bits)	Value
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gi 13967002 gb BG699072.1 BG699072	602678713F1 NIH_MGC_95 H...	1439 0.0
gi 14053781 gb BG743128.1 BG743128	602634270F1 NCI_CGAP_Skn...	1427 0.0
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gi 14047524 gb BG777207.1 BG777207	602664432F1 NIH_MGC_59 H...	1402 0.0
gi 13963233 gb BG697241.1 BG697241	602660481F1 NCI_CGAP_Skn...	1392 0.0
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gi 13336094 gb BG429588.1 BG429588	602501268F1 NIH_MGC_75 H...	1368 0.0
gi 9124275 gb BE253854.1 BE253854	601112818F1 NIH_MGC_16 Ho...	1364 0.0
gi 12604238 gb BG110732.1 BG110732	602279029F1 NIH_MGC_86 H...	1358 0.0
gi 13527202 gb BG535657.1 BG535657	602563366F1 NIH_MGC_77 H...	1344 0.0
gi 13289966 gb BG396518.1 BG396518	602459353F1 NIH_MGC_16 H...	1342 0.0
gi 14064290 gb BG753637.1 BG753637	602732827F1 NIH_MGC_43 H...	1330 0.0
gi 10156435 gb BE742443.1 BE742443	601575210F1 NIH_MGC_9 Ho...	1330 0.0
gi 13570738 gb BG563086.1 BG563086	602581878F1 NIH_MGC_76 H...	1314 0.0
gi 10399800 gb BE906369.1 BE906369	601498517F1 NIH_MGC_70 H...	1308 0.0
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gi 14565107 gb BI114206.1 BI114206	602862564F1 NIH_MGC_17 H...	1292 0.0
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gi 14566302 gb BI115401.1 BI115401	602863260F1 NIH_MGC_17 H...	1273 0.0
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gi 9179232 gb BE295680.1 BE295680	601175688F1 NIH_MGC_17 Ho...	1235 0.0
gi 13523981 gb BG532442.1 BG532442	602561968F1 NIH_MGC_61 H...	1227 0.0

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 gi|9323581|gb|BE378216.1|BE378216 601237991F1 NIH_MGC_44 Ho... 1140 0.0
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 gi|13458797|gb|BG497280.1|BG497280 602537844F1 NIH_MGC_59 H... 1128 0.0
 gi|9179583|gb|BE296026.1|BE296026 601175058F1 NIH_MGC_17 Ho... 1128 0.0
 gi|9770617|gb|BE541972.1|BE541972 601064273F1 NIH_MGC_10 Ho... 1126 0.0
 gi|12612166|gb|BG118660.1|BG118660 602348226F1 NIH_MGC_90 H... 1108 0.0
 gi|6568025|gb|AW235636.1|AW235636 xn20g09.x1 NCI_CGAP_Kid11... 1102 0.0
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 gi|11954238|gb|BF680343.1|BF680343 602154124F1 NIH_MGC_83 H... 1070 0.0
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 gi|14178068|gb|BG830481.1|BG830481 602767043F1 NIH_MGC_42 H... 1057 0.0
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gi|5364540|gb|AI799068.1|AI799068 we98b05.x1 Soares_NFL_T_G... 987 0.0
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>gi|7706523|ref|NP_057457.1| FOR II; WW domain-containing protein WWOX;
fragile site FRA16D oxidoreductase; putative oxidoreductase [Homo sapiens]

EST Search:

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gi 12788142 emb AL524649.1 AL524649 AL524649 LTI_NFL003_NBC...	1739	0.0
gi 12924548 emb AL569324.1 AL569324 AL569324 LTI_FL002_PL1 ...	1522	0.0
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gi 13980599 gb BG705846.1 BG705846 602669332F1 NIH_MGC_96 H...	1455	0.0
gi 14082760 gb BG772107.1 BG772107 602721554F1 NIH_MGC_97 H...	1398	0.0
gi 11643090 gb BF569710.1 BF569710 602186235F1 NIH_MGC_45 H...	1338	0.0
gi 5849973 gb AW002967.1 AW002967 wr03h08.x1 NCI_CGAP_GC6 H...	1328	0.0
gi 5886535 gb AW027779.1 AW027779 wv24d06.x1 NCI_CGAP_Kid11...	1326	0.0
gi 10316595 gb BE867819.1 BE867819 601443785F1 NIH_MGC_65 H...	1320	0.0
gi 10147851 gb BE733756.1 BE733756 601568287F1 NIH_MGC_21 H...	1314	0.0
gi 13735635 gb BG213932.1 BG213932 RST33572 Athersys RAGE L...	1308	0.0
gi 12910724 emb AL562371.1 AL562371 AL562371 LTI_NFL003_NBC...	1302	0.0
gi 5368521 gb AI803049.1 AI803049 tj60g08.x1 Soares_NSF_F8...	1296	0.0
gi 12766396 gb BG256580.1 BG256580 602370237F1 NIH_MGC_92 H...	1289	0.0
gi 12874081 emb AL542236.1 AL542236 AL542236 LTI_FL002_PL1 ...	1287	0.0
gi 13746217 gb BG220196.1 BG220196 RST39968 Athersys RAGE L...	1265	0.0
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gi 14568452 gb BI117551.1 BI117551 602866727F1 NIH_MGC_7 Ho...	1015	0.0
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gi|6946883|gb|AW418951.1|AW418951 ha24d04.x1 NCI_CGAP_Kid12... 874 0.0
gi|11687028|gb|BF594704.1|BF594704 7o54c01.x1 NCI_CGAP_Kid1... 870 0.0
gi|5812079|gb|AI984802.1|AI984802 wr85e01.x1 NCI_CGAP_Kid11... 862 0.0
gi|5707011|gb|AI942355.1|AI942355 wo80b08.x1 NCI_CGAP_Kid11... 827 0.0
gi|9512753|gb|BE466978.1|BE466978 hz59h08.x1 NCI_CGAP_Lu24 ... 815 0.0
gi|9260409|gb|BE348556.1|BE348556 ht71g08.x1 NCI_CGAP_Lu24 ... 815 0.0
gi|4985674|gb|AI697774.1|AI697774 we17b12.x1 NCI_CGAP_Lu24 ... 815 0.0
gi|10035137|gb|BE674596.1|BE674596 7e09c12.x1 NCI_CGAP_Lu24... 813 0.0
gi|3277850|gb|AI038656.1|AI038656 ox39e11.s1 Soares_total_f... 809 0.0
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>gi|4502599|ref|NP_001748.1| carbonyl reductase 1; carbonyl reductase (NADPH); carbonyl reductase (NADPH) 1 [Homo sapiens]

EST Search:

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gi 12932323 emb AL573258.1 AL573258 AL573258 LTI_NFL006_PL2...	1515	0.0
gi 12910574 emb AL562295.1 AL562295 AL562295 LTI_NFL003_NBC...	1513	0.0
gi 12878532 emb AL545910.1 AL545910 AL545910 LTI_NFL006_PL2...	1505	0.0
gi 14051000 gb BG740347.1 BG740347 602634102F1 NCI_CGAP_Skn...	1485	0.0
gi 13995976 gb BG716789.1 BG716789 602678195F1 NIH_MGC_96 H...	1483	0.0
gi 13913215 gb BG681818.1 BG681818 602629747F1 NCI_CGAP_Skn...	1473	0.0
gi 13409549 gb BG477270.1 BG477270 602523416F1 NIH_MGC_20 H...	1457	0.0
gi 14061754 gb BG751101.1 BG751101 602729893F1 NIH_MGC_43 H...	1445	0.0
gi 14567986 gb BI117085.1 BI117085 602867878F1 NIH_MGC_7 Ho...	1427	0.0
gi 13976186 gb BG703646.1 BG703646 602686612F1 NIH_MGC_95 H...	1421	0.0
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gi 12928754 emb AL571448.1 AL571448 AL571448 LTI_NFL006_PL2...	1382	0.0
gi 13986026 gb BG708561.1 BG708561 602670460F1 NIH_MGC_96 H...	1378	0.0
gi 12873034 emb AL541708.1 AL541708 AL541708 LTI_Fl002_PL1 ...	1366	0.0
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gi 10356604 gb BE894338.1 BE894338 601432922F1 NIH_MGC_72 H...	1346	0.0
gi 12097845 gb BF792860.1 BF792860 602253342F1 NIH_MGC_84 H...	1338	0.0
gi 12422069 gb BG031614.1 BG031614 602299760F1 NIH_MGC_87 H...	1336	0.0
gi 10205944 gb BE784746.1 BE784746 601473657F1 NIH_MGC_68 H...	1332	0.0
gi 13337465 gb BG430959.1 BG430959 602500260F1 NIH_MGC_75 H...	1330	0.0
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gi 11100906 gb BF207320.1 BF207320 601870527F1 NIH_MGC_19 H...	1320	0.0
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>gi|4502601|ref|NP_001227.1| carbonyl reductase 3; carbonyl reductase (NADPH) 3 [Homo sapiens]

EST Search:

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gi 7253791 gb AW578742.1 AW578742 RC1-CT0279-070100-021-h06... 825	0.0	
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>gi|5031737|ref|NP_005785.1| short-chain alcohol dehydrogenase family member [Homo sapiens]

EST Search:

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gi|14802614|gb|BI252296.1|BI252296 602953015F1 NIH_MGC_100 ... 1037 0.0
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gi|9150554|gb|BE275597.1|BE275597 601121106F1 NIH_MGC_20 Ho... 954 0.0
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gi|14803206|gb|BI252593.1|BI252593 602952582T1 NIH_MGC_100 ... 912 0.0
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gi|5663486|gb|AI927522.1|AI927522 wo90h11.x1 NCI_CGAP_Kid11... 894 0.0
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>gi|4504507|ref|NP_000853.1| hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid delta-isomerase 1; Hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid [Homo sapiens]

EST Search:

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gi 12877991 emb AL545509.1 AL545509 AL545509 LTI_NFL006_PL2...	1925	0.0
gi 12893183 emb AL553392.1 AL553392 AL553392 LTI_NFL006_PL2...	1911	0.0
gi 12895448 emb AL554554.1 AL554554 AL554554 LTI_NFL006_PL2...	1909	0.0
gi 12931487 emb AL572835.1 AL572835 AL572835 LTI_NFL006_PL2...	1905	0.0
gi 12940115 emb AL577210.1 AL577210 AL577210 LTI_NFL006_PL2...	1903	0.0
gi 12937740 emb AL576013.1 AL576013 AL576013 LTI_NFL006_PL2...	1871	0.0
gi 12882457 emb AL547931.1 AL547931 AL547931 LTI_NFL006_PL2...	1861	0.0
gi 12871910 emb AL541135.1 AL541135 AL541135 LTI_FL002_PL1 ...	1852	0.0
gi 12886860 emb AL550160.1 AL550160 AL550160 LTI_NFL006_PL2...	1850	0.0
gi 12938513 emb AL576403.1 AL576403 AL576403 LTI_NFL006_PL2...	1842	0.0
gi 12882827 emb AL548117.1 AL548117 AL548117 LTI_NFL006_PL2...	1838	0.0
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gi 12888448 emb AL550960.1 AL550960 AL550960 LTI_NFL006_PL2...	1808	0.0
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gi 12877435 emb AL544954.1 AL544954 AL544954 LTI_NFL006_PL2...	1754	0.0
gi 12877044 emb AL544564.1 AL544564 AL544564 LTI_NFL006_PL2...	1742	0.0
gi 12892145 emb AL552859.1 AL552859 AL552859 LTI_NFL006_PL2...	1719	0.0

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gi|13961102|gb|BG696201.1|BG696201 602659327F1 NCI_CGAP_Skn... 1281 0.0
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gi|12927889|emb|AL571013.1|AL571013 AL571013 LTI_NFL006_PL2... 1072 0.0
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>gi|4504509|ref|NP_000189.1| hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid delta-isomerase 2; Hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid [Homo sapiens]

EST Search:

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Sequences producing significant alignments:	(bits)	Value
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gi 12887155 emb AL550307.1 AL550307	AL550307 LTI_NFL006_PL2...	1400 0.0
gi 12877991 emb AL545509.1 AL545509	AL545509 LTI_NFL006_PL2...	1392 0.0
gi 12895448 emb AL554554.1 AL554554	AL554554 LTI_NFL006_PL2...	1374 0.0
gi 12893183 emb AL553392.1 AL553392	AL553392 LTI_NFL006_PL2...	1352 0.0
gi 12882457 emb AL547931.1 AL547931	AL547931 LTI_NFL006_PL2...	1334 0.0
gi 12871910 emb AL541135.1 AL541135	AL541135 LTI_FL002_PL1 ...	1332 0.0
gi 12886860 emb AL550160.1 AL550160	AL550160 LTI_NFL006_PL2...	1330 0.0
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gi 12882827 emb AL548117.1 AL548117	AL548117 LTI_NFL006_PL2...	1324 0.0
gi 12882752 emb AL548079.1 AL548079	AL548079 LTI_NFL006_PL2...	1316 0.0
gi 12895626 emb AL554645.1 AL554645	AL554645 LTI_NFL006_PL2...	1314 0.0
gi 12889651 emb AL551573.1 AL551573	AL551573 LTI_NFL006_PL2...	1294 0.0
gi 12888448 emb AL550960.1 AL550960	AL550960 LTI_NFL006_PL2...	1294 0.0
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gi 10730523 dbj AV711217.1 AV711217	AV711217 Cu Homo sapien...	1279 0.0
gi 10728926 dbj AV710297.1 AV710297	AV710297 Cu Homo sapien...	1275 0.0
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gi 10722430 dbj AV705124.1 AV705124	AV705124 ADB Homo sapie...	1257 0.0
gi 10730370 dbj AV711064.1 AV711064	AV711064 Cu Homo sapien...	1255 0.0
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gi 10730058 dbj AV710752.1 AV710752	AV710752 Cu Homo sapien...	1247 0.0
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 gi|10722640|dbj|AV705335.1|AV705335 AV705335 ADB Homo sapie... 1170 0.0
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 gi|10723870|dbj|AV706592.1|AV706592 AV706592 ADB Homo sapie... 1168 0.0
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>gi|4507185|ref|NP_003115.1| sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase); Sepiapterin reductase [Homo sapiens]

EST Search:

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gi|10396046|gb|BE904122.1|BE904122 601494330F2 NIH_MGC_70 H... 1318 0.0
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gi|1964997|gb|AA312648.1|AA312648 EST183324 Jurkat T-cells ... 797 0.0

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>gi|2338748|gb|AAB67236.1| oxidoreductase [Homo sapiens]

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>gi|4506359|ref|NP_000311.1| quinoid dihydropteridine reductase;
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>gi|4506571|ref|NP_003699.1| microsomal NAD+-dependent retinol dehydrogenase 4 [Homo sapiens]

EST Search:

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gi 13996568 gb BG717381.1 BG717381	602689723F1 NIH_MGC_97 H...	1404 0.0

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 gi|9896933|gb|BE615334.1|BE615334 601280732F1 NIH_MGC_39 Ho... 1211 0.0
 gi|12387354|gb|BF984542.1|BF984542 602307730F1 NIH_MGC_88 H... 1170 0.0
 gi|13717172|gb|BG195485.1|BG195485 RST14677 Athersys RAGE L... 1168 0.0
 gi|10401855|gb|BE907862.1|BE907862 601501989F1 NIH_MGC_70 H... 1166 0.0
 gi|12670948|gb|BG164245.1|BG164245 602341256F1 NIH_MGC_89 H... 1152 0.0
 gi|11331761|gb|BF369736.1|BF369736 QV4-GN0120-250900-427-c1... 1150 0.0
 gi|2321379|gb|AA551127.1|AA551127 nk75g03.s1 NCI_CGAP_Sch1 ... 1150 0.0
 gi|10744866|gb|BF036769.1|BF036769 601459836F1 NIH_MGC_66 H... 1146 0.0
 gi|13528208|gb|BG536662.1|BG536662 602566285F1 NIH_MGC_77 H... 1144 0.0
 gi|8147555|gb|AW957872.1|AW957872 EST369942 MAGE resequence... 1142 0.0
 gi|12344922|gb|BF977707.1|BF977707 602148324F1 NIH_MGC_62 H... 1130 0.0
 gi|11944012|gb|BF670117.1|BF670117 602119443F1 NIH_MGC_56 H... 1122 0.0
 gi|13546026|gb|BG547348.1|BG547348 602574782F1 NIH_MGC_77 H... 1118 0.0
 gi|12676722|gb|BG170019.1|BG170019 602323391F1 NIH_MGC_89 H... 1088 0.0
 gi|11649900|gb|BF576188.1|BF576188 602132627F1 NIH_MGC_81 H... 1078 0.0
 gi|14512380|gb|BI094050.1|BI094050 602860005F1 NIH_MGC_10 H... 1074 0.0
 gi|13050007|gb|BG291790.1|BG291790 602386010F1 NIH_MGC_93 H... 1068 0.0
 gi|13460516|gb|BG498986.1|BG498986 602544674F1 NIH_MGC_60 H... 1067 0.0
 gi|10796504|dbj|AV714987.1|AV714987 AV714987 DCB Homo sapie... 1065 0.0
 gi|12604885|gb|BG111281.1|BG111281 602283354F1 NIH_MGC_86 H... 1047 0.0
 gi|14049576|gb|BG779259.1|BG779259 602665938F1 NIH_MGC_60 H... 1045 0.0
 gi|11111634|gb|BF218048.1|BF218048 601882836F1 NIH_MGC_57 H... 1045 0.0
 gi|12383548|gb|BF980736.1|BF980736 602303884F1 NIH_MGC_88 H... 1035 0.0
 gi|14049921|gb|BG779604.1|BG779604 602668351F1 NIH_MGC_60 H... 1033 0.0
 gi|11252265|gb|BF305371.1|BF305371 601892847F1 NIH_MGC_17 H... 1021 0.0
 gi|13041668|gb|BG287637.1|BG287637 602384460F1 NIH_MGC_93 H... 1019 0.0
 gi|12677991|gb|BG171288.1|BG171288 602322318F1 NIH_MGC_89 H... 1015 0.0
 gi|4435867|gb|AI521732.1|AI521732 ti82c06.x1 NCI_CGAP_Kid11... 1007 0.0
 gi|7136231|gb|AW498488.1|AW498488 EST0021 Human Fetal Brain... 1001 0.0
 gi|12097334|gb|BF792280.1|BF792280 602252790F1 NIH_MGC_84 H... 991 0.0
 gi|1522055|gb|AA044198.1|AA044198 zk50e08.r1 Soares_pregnant... 991 0.0
 gi|14049653|gb|BG779336.1|BG779336 602665853F1 NIH_MGC_60 H... 973 0.0
 gi|14049581|gb|BG779264.1|BG779264 602665946F1 NIH_MGC_60 H... 961 0.0
 gi|1371208|gb|W63627.1|W63627 zc56f09.r1 Soares_parathyroid... 961 0.0
 gi|7136229|gb|AW498487.1|AW498487 EST0020 Human Fetal Brain... 959 0.0
 gi|11629318|gb|BF541849.1|BF541849 602069042F1 NIH_MGC_58 H... 954 0.0

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gi|14003292|gb|BG724105.1|BG724105 602697407F1 NIH_MGC_97 H... 950 0.0
 gi|14070365|gb|BG759712.1|BG759712 602711109F1 NIH_MGC_48 H... 940 0.0
 gi|1735571|gb|AA161274.1|AA161274 zq38f09.r1 Stratagene hNT... 940 0.0
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 gi|11112382|gb|BF218886.1|BF218886 601885044F1 NIH_MGC_57 H... 928 0.0
 gi|11977542|gb|BF692134.1|BF692134 602248727F1 NIH_MGC_62 H... 920 0.0
 gi|11767406|gb|BE963886.2|BE963886 601657654R1 NIH_MGC_68 H... 912 0.0
 gi|3920107|gb|AI281874.1|AI281874 qt68g10.x1 NCI_CGAP_Eso2 ... 910 0.0
 gi|10970869|gb|BF131829.1|BF131829 601820750F1 NIH_MGC_58 H... 906 0.0
 gi|13043036|gb|BG288319.1|BG288319 602383655F1 NIH_MGC_93 H... 900 0.0
 gi|12345982|gb|BF978767.1|BF978767 602149103F2 NIH_MGC_62 H... 898 0.0
 gi|5113976|gb|AI745688.1|AI745688 tr24h04.x1 NCI_CGAP_Ov23 ... 894 0.0
 gi|1694006|gb|AA132312.1|AA132312 zo17g05.s1 Stratagene col... 874 0.0
 gi|5875725|gb|AW022195.1|AW022195 df34b10.y1 Morton Fetal C... 870 0.0
 gi|2113174|gb|AA429830.1|AA429830 zw60g07.r1 Soares_total_f... 868 0.0
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 gi|11649499|gb|BF575787.1|BF575787 602134824F1 NIH_MGC_81 H... 858 0.0
 gi|12339937|gb|BF972722.1|BF972722 602240976F1 NIH_MGC_46 H... 856 0.0
 gi|5113967|gb|AI745679.1|AI745679 tr24g03.x1 NCI_CGAP_Ov23 ... 856 0.0
 gi|4486633|gb|AI554270.1|AI554270 tq05b03.x1 NCI_CGAP_Ut3 H... 852 0.0
 gi|9771262|gb|BE542617.1|BE542617 601067112F1 NIH_MGC_10 Ho... 848 0.0
 gi|7043218|gb|AW473112.1|AW473112 xp68h08.x2 NCI_CGAP_Ov39 ... 848 0.0
 gi|4372411|gb|AI479243.1|AI479243 tm56b07.x1 NCI_CGAP_Kid11... 844 0.0
 gi|1138607|gb|N24457.1|N24457 yx15a03.r1 Soares melanocyte ... 837 0.0
 gi|1577675|gb|AA070298.1|AA070298 zm68c06.r1 Stratagene neu... 831 0.0
 gi|8909315|gb|BE221906.1|BE221906 hu04d07.x1 NCI_CGAP_Lu24 ... 821 0.0
 gi|6975014|gb|AW439708.1|AW439708 hb87f06.x1 NCI_CGAP_Ut2 H... 809 0.0
 gi|12077114|gb|BF750438.1|BF750438 RC1-BN0410-261000-013-a0... 803 0.0
 gi|5232026|gb|AI765517.1|AI765517 wi81a05.x1 NCI_CGAP_Kid12... 803 0.0
 gi|4969797|gb|AI692457.1|AI692457 wd70f09.x1 NCI_CGAP_Lu24 ... 803 0.0
 gi|7667944|gb|AW753012.1|AW753012 QV0-CT0225-011199-041-h01... 801 0.0

>gi|3859946|gb|AAC72923.1| retinol dehydrogenase [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 9868612 dbj AV647598.1 AV647598 AV647598 GLC Homo sapien...	1041	0.0
gi 9868702 dbj AV647688.1 AV647688 AV647688 GLC Homo sapien...	1017	0.0
gi 9882195 dbj AV661181.1 AV661181 AV661181 GLC Homo sapien...	955	0.0
gi 9882144 dbj AV661130.1 AV661130 AV661130 GLC Homo sapien...	928	0.0
gi 7310181 gb AW605440.1 AW605440 PM1-DT0063-170100-002-h11...	880	0.0
gi 3432904 gb AI093928.1 AI093928 qa27e04.s1 Soares_NhHMPu...	825	0.0

>gi|8393516|ref|NP_057006.1| NAD(P) dependent steroid dehydrogenase-like; H105e3 [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 12798924 emb AL535431.1 AL535431 AL535431 LTI_FL013_FBrn...	1852	0.0
gi 12795943 emb AL532450.1 AL532450 AL532450 LTI_NFL001_NBC...	1800	0.0
gi 12798925 emb AL535432.1 AL535432 AL535432 LTI_FL013_FBrn...	1758	0.0

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gi|12783081;emb|AL519588.1|AL519588 AL519588 LTI_NFL004_NBC... 1721 0.0
gi|12791348;emb|AL527855.1|AL527855 AL527855 LTI_NFL003_NBC... 1687 0.0
gi|12787933;emb|AL524440.1|AL524440 AL524440 LTI_NFL003_NBC... 1639 0.0
gi|12783082;emb|AL519589.1|AL519589 AL519589 LTI_NFL004_NBC... 1614 0.0
gi|12914749;emb|AL564391.1|AL564391 AL564391 LTI_NFL001_NBC... 1590 0.0
gi|14051016;gb|BG740363.1|BG740363 602634122F1 NCI_CGAP_Skn... 1550 0.0
gi|12787932;emb|AL524439.1|AL524439 AL524439 LTI_NFL003_NBC... 1548 0.0
gi|12890777;emb|AL552152.1|AL552152 AL552152 LTI_NFL006_PL2... 1542 0.0
gi|13402737;gb|BG470462.1|BG470462 602511345F1 NIH_MGC_16 H... 1509 0.0
gi|14053579;gb|BG742926.1|BG742926 602632016F1 NCI_CGAP_Skn... 1487 0.0
gi|12791349;emb|AL527856.1|AL527856 AL527856 LTI_NFL003_NBC... 1475 0.0
gi|13995873;gb|BG716686.1|BG716686 602678065F1 NIH_MGC_96 H... 1469 0.0
gi|13969104;gb|BG700101.1|BG700101 602679482F1 NIH_MGC_95 H... 1453 0.0
gi|12912123;emb|AL563072.1|AL563072 AL563072 LTI_NFL003_NBC... 1447 0.0
gi|14620007;gb|BI160006.1|BI160006 602864207F1 NIH_MGC_42 H... 1439 0.0
gi|13287087;gb|BG393639.1|BG393639 602412043F1 NIH_MGC_92 H... 1384 0.0
gi|12098534;gb|BF793480.1|BF793480 602254967F1 NIH_MGC_84 H... 1366 0.0
gi|12347277;gb|BF980062.1|BF980062 602288651T1 NIH_MGC_97 H... 1360 0.0
gi|13450037;gb|BG488530.1|BG488530 602534430F1 NIH_MGC_18 H... 1344 0.0
gi|10321873;gb|BE873097.1|BE873097 601451595F1 NIH_MGC_65 H... 1342 0.0
gi|12936786;emb|AL575531.1|AL575531 AL575531 LTI_NFL006_PL2... 1336 0.0
gi|12098227;gb|BF793173.1|BF793173 602253005F1 NIH_MGC_84 H... 1332 0.0
gi|9894650;gb|BE613053.1|BE613053 601451936T1 NIH_MGC_66 Ho... 1324 0.0
gi|13994535;gb|BG715352.1|BG715352 602677379F1 NIH_MGC_96 H... 1322 0.0
gi|9893974;gb|BE612377.1|BE612377 601451936F1 NIH_MGC_66 Ho... 1300 0.0
gi|4740315;gb|AI656336.1|AI656336 tt44h04.x1 NCI_CGAP_GC6 H... 1298 0.0
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gi|4373215;gb|AI480047.1|AI480047 tm71e11.x1 NCI_CGAP_Brn25... 1138 0.0
gi|4289089;gb|AI433425.1|AI433425 ti65d04.x1 NCI_CGAP_Kid11... 1090 0.0
gi|11106808;gb|BF213222.1|BF213222 601844705F1 NIH_MGC_55 H... 1078 0.0
gi|10215890;gb|BE794692.1|BE794692 601590508F1 NIH_MGC_7 Ho... 1074 0.0
gi|14002691;gb|BG723504.1|BG723504 602694207F1 NIH_MGC_97 H... 1067 0.0
gi|8006977;gb|AW872924.1|AW872924 hq20a04.x1 NCI_CGAP_Adrl ... 1059 0.0
gi|10328016;gb|BE879240.1|BE879240 601486988F1 NIH_MGC_69 H... 1047 0.0
gi|12346975;gb|BF979760.1|BF979760 602288651F1 NIH_MGC_97 H... 1027 0.0
gi|8139772;gb|AW950007.1|AW950007 EST362197 MAGE resequence... 1011 0.0
gi|12901543;emb|AL557690.1|AL557690 AL557690 LTI_FL012_TC1 ... 1005 0.0
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gi|14649236;gb|BI194216.1|BI194216 602945971F1 NIH_MGC_42 H... 961 0.0
gi|13141924;gb|BG335486.1|BG335486 602403957F1 NIH_MGC_21 H... 946 0.0
gi|12132238;gb|BF803249.1|BF803249 IL5-CI0149-011100-224-h0... 934 0.0
gi|41111947;gb|AI360326.1|AI360326 qy89e03.x1 NCI_CGAP_Brn25... 930 0.0
gi|2162963;gb|AA448943.1|AA448943 zx07a07.r1 Soares_total_f... 926 0.0
gi|12070667;gb|BF743991.1|BF743991 RC0-BT0812-181000-035-a0... 916 0.0
gi|7913755;gb|AW820761.1|AW820761 RC5-ST0300-270300-014-B08... 916 0.0
gi|2411270;gb|AA595924.1|AA595924 nn15h12.s1 NCI_CGAP_Co12 ... 904 0.0
gi|1802687;gb|AA207195.1|AA207195 zq73h05.r1 Stratagene neu... 900 0.0

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gi|10829806|dbj|AV724928.1|AV724928 AV724928 HTB Homo sapie... 894 0.0
gi|3405877|gb|AI076699.1|AI076699 oz16f12.x1 Soares_fetal_I... 872 0.0
gi|14471711|gb|BI064184.1|BI064184 IL3-UT0119-180401-476-B0... 870 0.0
gi|5130990|gb|AI752726.1|AI752726 cn18d06.y1 Normal Human T... 839 0.0
gi|3418300|gb|AI081508.1|AI081508 oz53h08.x1 Soares_senesce... 833 0.0
gi|9323549|gb|BE378184.1|BE378184 601237939F1 NIH_MGC_44 Ho... 827 0.0
gi|10719367|dbj|AV703037.1|AV703037 AV703037 ADB Homo sapie... 823 0.0
gi|3434745|gb|AI095769.1|AI095769 qb30c05.x1 Soares_pregnant... 815 0.0

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>gi|7661658|ref|NP_056325.1| DKFZP566O084 protein [Homo sapiens]

EST Search:

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gi 15019948 gb BI335291.1 BI335291	602998213F1 NIH_MGC_12 H...	1463 0.0
gi 10219393 gb BE798195.1 BE798195	601582662F1 NIH_MGC_7 Ho...	1411 0.0
gi 10156033 gb BE742041.1 BE742041	601594721F1 NIH_MGC_9 Ho...	1400 0.0
gi 10150854 gb BE736951.1 BE736951	601306912F1 NIH_MGC_39 H...	1392 0.0
gi 10216541 gb BE795343.1 BE795343	601586662F1 NIH_MGC_7 Ho...	1376 0.0
gi 12678574 gb BG171871.1 BG171871	602322675F1 NIH_MGC_89 H...	1279 0.0
gi 9331772 gb BE386407.1 BE386407	601273578F1 NIH_MGC_20 Ho...	1249 0.0
gi 9148949 gb BE274012.1 BE274012	601104628F1 NIH_MGC_14 Ho...	1239 0.0
gi 9334357 gb BE388992.1 BE388992	601284814F1 NIH_MGC_44 Ho...	1229 0.0
gi 9335068 gb BE389703.1 BE389703	601281945F1 NIH_MGC_44 Ho...	1172 0.0
gi 13409767 gb BG477488.1 BG477488	602521540F1 NIH_MGC_20 H...	1164 0.0
gi 10206923 gb BE785725.1 BE785725	601475291F1 NIH_MGC_68 H...	1160 0.0
gi 14073190 gb BG762537.1 BG762537	602733994F1 NIH_MGC_49 H...	1098 0.0
gi 9335871 gb BE390506.1 BE390506	601284123F1 NIH_MGC_44 Ho...	1072 0.0
gi 1383218 gb W73084.1 W73084	zd54a11.r1 Soares_fetal_heart...	952 0.0
gi 5674161 gb AI935291.1 AI935291	wp16e06.x1 NCI_CGAP_Lu19 ...	924 0.0
gi 844959 gb R71442.1 R71442	yi51f01.r1 Soares_placenta Nb2...	908 0.0
gi 1163805 gb N40260.1 N40260	yx99g06.r1 Soares_melanocyte ...	892 0.0
gi 5920966 gb AW055263.1 AW055263	wz16b09.x1 NCI_CGAP_Ut4 H...	872 0.0
gi 12240526 gb BF852782.1 BF852782	MR3-EN0087-151200-012-f0...	864 0.0
gi 1319356 gb W37623.1 W37623	zc12d10.r1 Soares_parathyroid...	839 0.0
gi 1319173 gb W37568.1 W37568	zc10c03.r1 Soares_parathyroid...	821 0.0

>gi|12804999|gb|AAH01953.1|AAH01953 oxidoreductase UCPA [Homo sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
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gi 12793625 emb AL530132.1 AL530132	AL530132 LTI_NFL001_NBC...	1481 0.0
gi 12936195 emb AL575230.1 AL575230	AL575230 LTI_NFL006_PL2...	1477 0.0
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gi 13452667 gb BG491155.1 BG491155	602518792F1 NIH_MGC_18 H...	1392 0.0
gi 14051133 gb BG740480.1 BG740480	602633875F1 NCI_CGAP_Skn...	1390 0.0
gi 13982652 gb BG706873.1 BG706873	602672037F1 NIH_MGC_96 H...	1378 0.0
gi 3281013 gb AI041819.1 AI041819	oy34a10.x1 Soares_parathy...	1354 0.0
gi 13545674 gb BG547009.1 BG547009	602573805F1 NIH_MGC_77 H...	1336 0.0
gi 12793624 emb AL530131.1 AL530131	AL530131 LTI_NFL001_NBC...	1336 0.0
gi 13976480 gb BG703780.1 BG703780	602686804F1 NIH_MGC_95 H...	1328 0.0
gi 13039621 gb BG286600.1 BG286600	602381608F1 NIH_MGC_93 H...	1304 0.0
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gi 12598260 gb BG104418.1 BG104418	602311036F1 NIH_MGC_20 H...	1291 0.0
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gi|2877836|gb|AA808430.1|AA808430 oe53b08.s1 NCI_CGAP_Lu5 H... 1209 0.0
gi|6471396|gb|AW192697.1|AW192697 xl48h04.x1 NCI_CGAP_Pan1 ... 1193 0.0
gi|12910323|emb|AL562168.1|AL562168 AL562168 LTI_NFL003_NBC... 1178 0.0
gi|9186202|gb|BE302454.1|BE302454 ba65f04.y1 NIH_MGC_20 Hom... 1164 0.0
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gi|5109073|gb|AI740785.1|AI740785 wg24b10.x1 Soares_NSF_F8... 1138 0.0
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gi|8750771|gb|BE207373.1|BE207373 ba65e04.x1 NIH_MGC_20 Hom... 1063 0.0
gi|2993433|gb|AA883903.1|AA883903 aj13a01.s1 Soares_parathy... 1061 0.0
gi|3255193|gb|AI034240.1|AI034240 ow09h12.x1 Soares_parathy... 1059 0.0
gi|10350081|gb|BE891095.1|BE891095 601432208F1 NIH_MGC_72 H... 1053 0.0
gi|8750775|gb|BE207377.1|BE207377 ba65f04.x1 NIH_MGC_20 Hom... 1035 0.0
gi|5858190|gb|AW009412.1|AW009412 ws82c11.x1 NCI_CGAP_Co3 H... 1035 0.0
gi|5546002|gb|AI871953.1|AI871953 wrm53h05.x1 NCI_CGAP_Ut2 H... 1029 0.0
gi|2324986|gb|AA554447.1|AA554447 nl14h10.s1 NCI_CGAP_Br2 H... 1027 0.0
gi|4598887|gb|AI589839.1|AI589839 tm81a02.x1 NCI_CGAP_Bm25... 1017 0.0
gi|6200155|gb|AW152255.1|AW152255 xg40e03.x1 NCI_CGAP_Ut1 H... 1015 0.0
gi|2955773|gb|AA863294.1|AA863294 og93b12.s1 NCI_CGAP_Kid5 ... 1015 0.0
gi|2690528|gb|AA689601.1|AA689601 nv66b12.s1 NCI_CGAP_GCB1 ... 1013 0.0
gi|4834180|gb|AI669406.1|AI669406 ty32b07.x1 NCI_CGAP_Ut2 H... 1007 0.0
gi|9866597|dbj|AV645583.1|AV645583 AV645583 GLC Homo sapien... 999 0.0
gi|3001833|gb|AA886725.1|AA886725 oj52h06.s1 NCI_CGAP_Kid3 ... 999 0.0
gi|13546020|gb|BG547368.1|BG547368 602574776F1 NIH_MGC_77 H... 997 0.0
gi|13294752|gb|BG401304.1|BG401304 602465415F1 NIH_MGC_75 H... 997 0.0
gi|10367680|gb|BE855542.1|BE855542 7g15h08.x1 NCI_CGAP_Bm2... 995 0.0
gi|3086555|gb|AA932317.1|AA932317 oo70g12.s1 NCI_CGAP_GC4 H... 993 0.0
gi|3057816|gb|AA917926.1|AA917926 ol76h08.s1 NCI_CGAP_Kid3 ... 991 0.0
gi|9260891|gb|BE349038.1|BE349038 ht48c06.x1 NCI_CGAP_Mel15... 989 0.0
gi|5110966|gb|AI742678.1|AI742678 wg44h01.x1 Soares_NSF_F8... 987 0.0
gi|2411344|gb|AA595998.1|AA595998 nn64h09.s1 NCI_CGAP_Lar1 ... 987 0.0
gi|11129201|gb|BF222024.1|BF222024 7p41b04.x1 NCI_CGAP_Pr28... 985 0.0
gi|10891010|gb|BF085209.1|BF085209 MR3-GN0029-110900-004-h0... 983 0.0
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gi|5661371|gb|AI925407.1|AI925407 wo20h04.x1 NCI_CGAP_Pan1 ... 979 0.0
gi|1320910|gb|W39201.1|W39201 zb35h02.r1 Soares_parathyroid... 979 0.0
gi|4085247|gb|AI348041.1|AI348041 qp56b07.x1 NCI_CGAP_Co8 H... 975 0.0
gi|13336418|gb|BG429912.1|BG429912 602499351F1 NIH_MGC_75 H... 969 0.0
gi|2875248|gb|AA806498.1|AA806498 oc23f11.s1 NCI_CGAP_GCB1 ... 967 0.0
gi|2156117|gb|AA443442.1|AA443442 zw94c04.r1 Soares_total_f... 967 0.0
gi|7412910|gb|AW651660.1|AW651660 ba17d12.y2 NIH_MGC_35 Hom... 965 0.0
gi|3155485|gb|AA978039.1|AA978039 oq55e12.s1 NCI_CGAP_Kid5 ... 965 0.0
gi|13340888|gb|BG434382.1|BG434382 602506384F1 NIH_MGC_79 H... 961 0.0
gi|5592517|gb|AI887353.1|AI887353 wrm39c04.x1 NCI_CGAP_Ut4 H... 961 0.0
gi|3645373|gb|AI139401.1|AI139401 qc29a10.x1 Soares_pregnant... 961 0.0
gi|4075385|gb|AI338458.1|AI338458 qq92d04.x1 Soares_total_f... 959 0.0
gi|14083867|gb|BG773214.1|BG773214 602721957F1 NIH_MGC_97 H... 955 0.0
gi|3155394|gb|AA977948.1|AA977948 oq60h10.s1 NCI_CGAP_Kid6 ... 955 0.0
gi|2155983|gb|AA443308.1|AA443308 zw94c04.s1 Soares_total_f... 955 0.0
gi|13337258|gb|BG430752.1|BG430752 602498512F1 NIH_MGC_75 H... 950 0.0

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gi|13964507|gb|BG697842.1|BG697842 602661052F1 NCI_CGAP_Skn... 948 0.0
 gi|3281636|gb|AI042442.1|AI042442 oy14a03.x1 Soares_senesce... 944 0.0
 gi|3179412|gb|AA992867.1|AA992867 ot76b02.s1 Soares_total_f... 940 0.0
 gi|6302223|gb|AW163190.1|AW163190 au92h07.y1 Schneider feta... 934 0.0
 gi|3423724|gb|AI085301.1|AI085301 qf18g03.x1 NCI_CGAP_Bm25... 934 0.0
 gi|3017217|gb|AA890338.1|AA890338 aj94a11.s1 Soares_parathy... 932 0.0
 gi|12925499|emb|AL569800.1|AL569800 AL569800 LTINFL006_PL2... 928 0.0
 gi|10994439|dbj|AU133900.1|AU133900 AU133900 OVARC1 Homo sa... 928 0.0
 gi|11016587|dbj|AU155066.1|AU155066 AU155066 OVARC1 Homo sa... 926 0.0
 gi|3871543|gb|AI263340.1|AI263340 qq87h07.x1 Soares_total_f... 926 0.0
 gi|2359920|gb|AA582560.1|AA582560 nn55c06.s1 NCI_CGAP_Kid6 ... 920 0.0
 gi|1281745|gb|W07723.1|W07723 zb03b03.r1 Soares_fetal_lung_... 914 0.0
 gi|2941643|gb|AA854105.1|AA854105 aj71a02.s1 Soares_parathy... 908 0.0
 gi|12897527|emb|AL555621.1|AL555621 AL555621 LTINFL006_PL2... 886 0.0
 gi|12875635|emb|AL543157.1|AL543157 AL543157 LTINFL006_PL2... 878 0.0
 gi|12873084|emb|AL541734.1|AL541734 AL541734 LTIFL002_PL1 ... 876 0.0
 gi|9768144|gb|BE539499.1|BE539499 601060187F1 NIH_MGC_10 Ho... 874 0.0
 gi|14653349|gb|BI198328.1|BI198328 602761334F1 NIH_MGC_19 H... 868 0.0
 gi|11263603|gb|BF315365.1|BF315365 601902650F1 NIH_MGC_19 H... 868 0.0
 gi|12875843|emb|AL543365.1|AL543365 AL543365 LTINFL006_PL2... 864 0.0
 gi|14653113|gb|BI198092.1|BI198092 602762295F1 NIH_MGC_19 H... 852 0.0
 gi|5665179|gb|AI929215.1|AI929215 au58e05.x1 Schneider feta... 848 0.0
 gi|3241454|gb|AI025841.1|AI025841 ow12b07.s1 Soares_parathy... 848 0.0

>gi|4507709|ref|NP_003304.1| tissue specific transplantation antigen P35B;
 p35B; tissue specific transplantation antigen 3; Tissue-specific transplantation
 antigen-3; GDP-4-keto-6-deoxy-D-mannose epimerase-reductase [Homo
 sapiens]

EST Search:

Sequences producing significant alignments:	(bits)	Value
gi 12883797 emb AL548615.1 AL548615 AL548615 LTINFL006_PL2... 1772 0.0	1772	0.0
gi 12789331 emb AL525838.1 AL525838 AL525838 LTINFL003_NBC... 1752 0.0	1752	0.0
gi 13905346 gb BG673954.1 BG673954 602620125F1 NCI_CGAP_Skn... 1649 0.0	1649	0.0
gi 12792036 emb AL528543.1 AL528543 AL528543 LTINFL001_NBC... 1628 0.0	1628	0.0
gi 12789378 emb AL525885.1 AL525885 AL525885 LTINFL003_NBC... 1620 0.0	1620	0.0
gi 14060819 gb BG750166.1 BG750166 602708953F1 NIH_MGC_43 H... 1580 0.0	1580	0.0
gi 13584011 gb BG576358.1 BG576358 602597077F1 NIH_MGC_87 H... 1576 0.0	1576	0.0
gi 14808128 gb BI255073.1 BI255073 602975916F1 NIH_MGC_12 H... 1532 0.0	1532	0.0
gi 12932173 emb AL573182.1 AL573182 AL573182 LTINFL006_PL2... 1520 0.0	1520	0.0
gi 14170351 gb BG822764.1 BG822764 602725927F1 NIH_MGC_15 H... 1501 0.0	1501	0.0
gi 13582297 gb BG574644.1 BG574644 602596643F1 NIH_MGC_87 H... 1491 0.0	1491	0.0
gi 14504443 gb BI086113.1 BI086113 602870179T1 NIH_MGC_98 H... 1465 0.0	1465	0.0
gi 13031499 gb BG282607.1 BG282607 602406274F1 NIH_MGC_91 H... 1425 0.0	1425	0.0
gi 13987738 gb BG709420.1 BG709420 602673472F1 NIH_MGC_96 H... 1419 0.0	1419	0.0
gi 11974033 gb BF688625.1 BF688625 602185261F1 NIH_MGC_43 H... 1390 0.0	1390	0.0
gi 4997719 gb AI707943.1 AI707943 as34g07.x1 Barstead aorta... 1372 0.0	1372	0.0
gi 10153576 gb BE739584.1 BE739584 601556554T1 NIH_MGC_58 H... 1362 0.0	1362	0.0
gi 14050417 gb BG739764.1 BG739764 602630479F1 NCI_CGAP_Skn... 1356 0.0	1356	0.0
gi 12347310 gb BF980095.1 BF980095 602288690T1 NIH_MGC_97 H... 1338 0.0	1338	0.0
gi 11974420 gb BF689012.1 BF689012 602185261T1 NIH_MGC_43 H... 1330 0.0	1330	0.0
gi 14000222 gb BG721035.1 BG721035 602692740F1 NIH_MGC_97 H... 1326 0.0	1326	0.0
gi 12912349 emb AL563185.1 AL563185 AL563185 LTINFL001_NBC... 1298 0.0	1298	0.0
gi 6473452 gb AW194598.1 AW194598 xn42b05.x1 NCI_CGAP_Kid11... 1285 0.0	1285	0.0

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gi|12384107|gb|BF981295.1|BF981295 602308539F1 NIH_MGC_88 H... 1283 0.0
gi|5745797|gb|AI953487.1|AI953487 wq29c04.x1 NCI_CGAP_Kid11... 1281 0.0
gi|12418870|gb|BG029773.1|BG029773 602296507F1 NIH_MGC_87 H... 1279 0.0
gi|10812855|gb|BF058959.1|BF058959 7k36d11.x1 NCI_CGAP_Ov18... 1279 0.0
gi|5037850|gb|AI720594.1|AI720594 as70e02.x1 Barstead colon... 1269 0.0
gi|13129704|gb|BG323267.1|BG323267 602421494F1 NIH_MGC_14 H... 1267 0.0
gi|14177350|gb|BG829763.1|BG829763 602764240F1 NIH_MGC_42 H... 1265 0.0
gi|13404586|gb|BG472311.1|BG472311 602513954F1 NIH_MGC_16 H... 1259 0.0
gi|9346533|gb|BE410083.1|BE410083 601302232F1 NIH_MGC_21 Ho... 1259 0.0
gi|4684533|gb|AI633203.1|AI633203 tz07e05.x1 NCI_CGAP_Ut1 H... 1259 0.0
gi|14677298|gb|BI223854.1|BI223854 602942773F1 NIH_MGC_12 H... 1255 0.0
gi|4764562|gb|AI660979.1|AI660979 wf20f11.x1 Soares_Dieckgr... 1253 0.0
gi|13329564|gb|BG423058.1|BG423058 602450261F1 NIH_MGC_14 H... 1247 0.0
gi|11250503|gb|BF303843.1|BF303843 601886640F2 NIH_MGC_17 H... 1241 0.0
gi|5593865|gb|AI888701.1|AI888701 wn34f08.x1 NCI_CGAP_Gas4 ... 1231 0.0
gi|8905436|gb|BE218030.1|BE218030 hv34e04.x1 NCI_CGAP_Lu24 ... 1227 0.0
gi|11971550|gb|BF686142.1|BF686142 602143377F1 NIH_MGC_46 H... 1225 0.0
gi|11130839|gb|BF223661.1|BF223661 7q78e07.x1 NCI_CGAP_Lu24... 1223 0.0
gi|14503965|gb|BI085635.1|BI085635 602870179F1 NIH_MGC_98 H... 1217 0.0
gi|12342081|gb|BF974866.1|BF974866 602245527F1 NIH_MGC_48 H... 1207 0.0
gi|12339751|gb|BF972536.1|BF972536 602242932F1 NIH_MGC_46 H... 1203 0.0
gi|10316825|gb|BE868049.1|BE868049 601444153F1 NIH_MGC_65 H... 1195 0.0
gi|13342831|gb|BG436325.1|BG436325 602508768F1 NIH_MGC_79 H... 1193 0.0
gi|13459197|gb|BG497680.1|BG497680 601859714F1 NIH_MGC_60 H... 1187 0.0
gi|13414805|gb|BG482526.1|BG482526 602527765F1 NIH_MGC_21 H... 1185 0.0
gi|14294354|gb|BG913878.1|BG913878 602810511F1 NCI_CGAP_Bm... 1183 0.0
gi|13451814|gb|BG490304.1|BG490304 602519301F1 NIH_MGC_18 H... 1181 0.0
gi|7704180|gb|AW772117.1|AW772117 hn67f10.x1 NCI_CGAP_Kid11... 1172 0.0
gi|12762969|gb|BG253153.1|BG253153 602363796F1 NIH_MGC_90 H... 1170 0.0
gi|6590433|gb|AW247440.1|AW247440 2819332.5prime NIH_MGC_7 ... 1162 0.0
gi|12603972|gb|BG110466.1|BG110466 602278881F1 NIH_MGC_86 H... 1160 0.0
gi|12426963|gb|BG034049.1|BG034049 602300978F1 NIH_MGC_87 H... 1158 0.0
gi|11443051|gb|BF431015.1|BF431015 7o18a05.x1 NCI_CGAP_Kid1... 1156 0.0
gi|9339602|gb|BE394237.1|BE394237 601311549F1 NIH_MGC_44 Ho... 1146 0.0
gi|6361205|gb|AI174814.1|AI174814 HA2535 Human fetal liver ... 1138 0.0
gi|10389807|gb|BE901034.1|BE901034 601674169F1 NIH_MGC_21 H... 1130 0.0
gi|2933350|gb|AA845591.1|AA845591 ak04g03.s1 Soares_parathy... 1106 0.0
gi|12725613|gb|BG230580.1|BG230580 naf40f04.x1 Soares_NPBMC... 1104 0.0
gi|11263814|gb|BF315551.1|BF315551 601899689F1 NIH_MGC_19 H... 1104 0.0
gi|9346913|gb|BE410463.1|BE410463 601302064F1 NIH_MGC_21 Ho... 1102 0.0
gi|4851563|gb|AI671832.1|AI671832 wb34e03.x1 NCI_CGAP_GC6 H... 1102 0.0
gi|2409463|gb|AA594113.1|AA594113 nm81f09.s1 NCI_CGAP_Co9 H... 1102 0.0
gi|6590289|gb|AW247296.1|AW247296 2819332.3prime NIH_MGC_7 ... 1096 0.0
gi|14252587|gb|BG875594.1|BG875594 RC0-CN0025-010200-012-h0... 1088 0.0
gi|6660479|gb|AW273449.1|AW273449 xr39g05.x1 NCI_CGAP_Ut4 H... 1068 0.0
gi|12344867|gb|BF9777652.1|BF9777652 602147454F1 NIH_MGC_62 H... 1059 0.0
gi|5767006|gb|AI970180.1|AI970180 wr08c02.x1 NCI_CGAP_Lu19 ... 1045 0.0
gi|9154860|gb|BE279864.1|BE279864 601157218F1 NIH_MGC_21 Ho... 1043 0.0
gi|6043887|gb|AW088082.1|AW088082 xc97c12.x1 NCI_CGAP_Bm35... 1041 0.0
gi|5660644|gb|AI924680.1|AI924680 wn74c04.x1 NCI_CGAP_Ut1 H... 1041 0.0
gi|7320037|gb|AW614851.1|AW614851 hh67d09.x1 NCI_CGAP_GU1 H... 1005 0.0
gi|14374439|gb|BG956268.1|BG956268 QV3-CT0616-190201-553-f1... 993 0.0
gi|5368755|gb|AI803283.1|AI803283 tc17c01.x1 Soares_NhHMPu... 989 0.0
gi|14569068|gb|BI118167.1|BI118167 602867450F1 NIH_MGC_7 Ho... 977 0.0
gi|7319620|gb|AW614434.1|AW614434 hg83c06.x1 NCI_CGAP_Kid1... 973 0.0
gi|7044918|gb|AW474812.1|AW474812 xy20e11.x1 NCI_CGAP_Ut4 H... 973 0.0
gi|11983366|gb|BF697958.1|BF697958 602130044F1 NIH_MGC_56 H... 963 0.0

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gi|7376393|gb|AW629603.1|AW629603 hh67d09.y1 NCI_CGAP_GU1 H... 961 0.0
gi|12908174|emb|AL561089.1|AL561089 AL561089 LTI_NFL010_BC2... 957 0.0
gi|3214460|gb|AI004950.1|AI004950 ot98b10.x1 Soares_total_f... 957 0.0
gi|3756666|gb|AI204060.1|AI204060 qe77h04.x1 Soares_fetal_l... 944 0.0
gi|10964119|gb|BF125079.1|BF125079 601762687F1 NIH_MGC_20 H... 936 0.0
gi|13032697|gb|BG283127.1|BG283127 602406778F1 NIH_MGC_91 H... 932 0.0
gi|13410684|gb|BG478405.1|BG478405 602523747F1 NIH_MGC_20 H... 928 0.0
gi|13030280|gb|BG281355.1|BG281355 602401842F1 NIH_MGC_20 H... 926 0.0
gi|5101285|gb|AI739304.1|AI739304 wi30c03.x1 NCI_CGAP_Co16 ... 924 0.0
gi|3754557|gb|AI201951.1|AI201951 qs77a10.x1 NCI_CGAP_Pr28 ... 922 0.0
gi|8140882|gb|AW951214.1|AW951214 EST363284 MAGE resequence... 920 0.0
gi|12042881|gb|BF726970.1|BF726970 by14h02.y1 Human Lens cD... 918 0.0
gi|7150886|gb|AW512808.1|AW512808 xm04b07.x1 NCI_CGAP_Ut1 H... 916 0.0
gi|9334131|gb|BE388766.1|BE388766 601283865F1 NIH_MGC_44 Ho... 904 0.0
gi|4149912|gb|AI371159.1|AI371159 ta09b06.x1 Soares_total_f... 892 0.0
gi|14505970|gb|BI087640.1|BI087640 602852161F1 NIH_MGC_10 H... 890 0.0
gi|4662870|gb|AI626070.1|AI626070 ar87f06.x1 Barstead colon... 890 0.0
gi|3693002|gb|AI160843.1|AI160843 qb65e01.x1 Soares_fetal_h... 888 0.0
gi|3400763|gb|AI074119.1|AI074119 oz54c02.x1 Soares_senesce... 884 0.0
gi|3735843|gb|AI185205.1|AI185205 qe47a05.x1 Soares_fetal_l... 882 0.0

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Table 2: Mouse-SDRs derived from non redundant NCBI Database

EST Searches in human tissue

>gi|5668733|dbj|BAA82656.1| UBE-1a [Mus musculus]

EST Search:

Organ: eye

Tissue type: retinoblastoma

Organ: brain

Tissue type: hippocampus

Organ: ovary

Tissue type: adenocarcinoma cell line

Organ: bone

Tissue type: osteosarcoma, cell line

Human Sequences producing significant alignments:	(bits)	Value
--	--------	-------

gi 9124275 gb BE253854.1 BE253854 601112818F1 NIH_MGC_16 Ho...	454	e-125
gi 13967002 gb BG699072.1 BG699072 602678713F1 NIH_MGC_95 H...	430	e-118
gi 10156435 gb BE742443.1 BE742443 601575210F1 NIH_MGC_9 Ho...	428	e-117
gi 12604238 gb BG110732.1 BG110732 602279029F1 NIH_MGC_86 H...	418	e-114
gi 13401922 gb BG469647.1 BG469647 602534103F1 NIH_MGC_15 H...	412	e-112
gi 12609069 gb BG115563.1 BG115563 602317253F1 NIH_MGC_88 H...	412	e-112
gi 9186637 gb BE302889.1 BE302889 ba70g10.y1 NIH_MGC_20 Hom...	406	e-111
gi 12761697 gb BG251881.1 BG251881 602364502F1 NIH_MGC_90 H...	402	e-109
gi 14809963 gb BI255993.1 BI255993 602976353F1 NIH_MGC_12 H...	394	e-107
gi 12678524 gb BG171821.1 BG171821 602322603F1 NIH_MGC_89 H...	393	e-106
gi 10160188 gb BE746196.1 BE746196 601578644F1 NIH_MGC_9 Ho...	391	e-106
gi 12687397 gb BG180694.1 BG180694 602329481F1 NIH_MGC_91 H...	373	e-100
gi 13336094 gb BG429588.1 BG429588 602501268F1 NIH_MGC_75 H...	371	e-100
gi 8144363 gb AW954680.1 AW954680 EST366750 MAGE resequence...	371	e-100
gi 13999085 gb BG719898.1 BG719898 602691430F1 NIH_MGC_97 H...	357	7e-96
gi 11953928 gb BF680033.1 BF680033 602154752F1 NIH_MGC_83 H...	357	7e-96
gi 13972135 gb BG701616.1 BG701616 602682503F1 NIH_MGC_95 H...	345	3e-92
gi 10348906 gb BE890514.1 BE890514 601431585F1 NIH_MGC_72 H...	345	3e-92
gi 13969001 gb BG700048.1 BG700048 602681055F1 NIH_MGC_95 H...	343	1e-91
gi 9770617 gb BE541972.1 BE541972 601064273F1 NIH_MGC_10 Ho...	331	4e-88

>gi|5668735|dbj|BAA82657.1| UBE-1b [Mus musculus]

EST Search:

Organ: eye

Tissue type: retinoblastoma

Organ: ovary

Tissue type: adenocarcinoma cell line

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Organ: brain
 Tissue type: hippocampus

Organ: colon
 Tissue type: adenocarcinoma cell line

Human Sequences producing significant alignments: (bits) Value

gi 9124275 gb BE253854.1 BE253854	601112818F1 NIH_MGC_16 Ho...	438	e-120
gi 10156435 gb BE742443.1 BE742443	601575210F1 NIH_MGC_9 Ho...	412	e-112
gi 13967002 gb BG699072.1 BG699072	602678713F1 NIH_MGC_95 H...	400	e-109
gi 13401922 gb BG469647.1 BG469647	602534103F1 NIH_MGC_15 H...	396	e-108
gi 12604238 gb BG110732.1 BG110732	602279029F1 NIH_MGC_86 H...	389	e-105
gi 12761697 gb BG251881.1 BG251881	602364502F1 NIH_MGC_90 H...	387	e-105
gi 12609069 gb BG115563.1 BG115563	602317253F1 NIH_MGC_88 H...	383	e-103
gi 14809963 gb BI255993.1 BI255993	602976353F1 NIH_MGC_12 H...	379	e-102
gi 9186637 gb BE302889.1 BE302889	ba70g10.y1 NIH_MGC_20 Hom...	377	e-102
gi 10160188 gb BE746196.1 BE746196	601578644F1 NIH_MGC_9 Ho...	375	e-101
gi 12678524 gb BG171821.1 BG171821	602322603F1 NIH_MGC_89 H...	369	2e-99
gi 8144363 gb AW954680.1 AW954680	EST366750 MAGE resequence...	355	3e-95
gi 12687397 gb BG180694.1 BG180694	602329481F1 NIH_MGC_91 H...	349	2e-93
gi 13336094 gb BG429588.1 BG429588	602501268F1 NIH_MGC_75 H...	341	4e-91
gi 13999085 gb BG719898.1 BG719898	602691430F1 NIH_MGC_97 H...	327	7e-87
gi 11953928 gb BF680033.1 BF680033	602154752F1 NIH_MGC_83 H...	327	7e-87
gi 10348906 gb BE890514.1 BE890514	601431585F1 NIH_MGC_72 H...	323	1e-85
gi 13972135 gb BG701616.1 BG701616	602682503F1 NIH_MGC_95 H...	315	3e-83
gi 14053553 gb BG742900.1 BG742900	602632481F1 NCI_CGAP_Skn...	313	1e-82
gi 9770617 gb BE541972.1 BE541972	601064273F1 NIH_MGC_10 Ho...	305	2e-80

>gi|12835589|dbj|BAB23296.1| putative [Mus musculus]

EST Search:

Organ: eye
 Tissue type: retinoblastoma

Organ: brain
 Tissue type: hippocampus

Organ: ovary
 Tissue type: adenocarcinoma cell line

Organ: bone
 Tissue type: osteosarcoma, cell line

Human Sequences producing significant alignments: (bits) Value

gi 9124275 gb BE253854.1 BE253854	601112818F1 NIH_MGC_16 Ho...	454	e-125
gi 13967002 gb BG699072.1 BG699072	602678713F1 NIH_MGC_95 H...	430	e-118
gi 10156435 gb BE742443.1 BE742443	601575210F1 NIH_MGC_9 Ho...	428	e-117
gi 12604238 gb BG110732.1 BG110732	602279029F1 NIH_MGC_86 H...	418	e-114
gi 13401922 gb BG469647.1 BG469647	602534103F1 NIH_MGC_15 H...	412	e-112
gi 12609069 gb BG115563.1 BG115563	602317253F1 NIH_MGC_88 H...	412	e-112

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gi|9186637|gb|BE302889.1|BE302889 ba70g10.y1 NIH_MGC_20 Hom... 406 e-111
 gi|12761697|gb|BG251881.1|BG251881 602364502F1 NIH_MGC_90 H... 402 e-109
 gi|14809963|gb|BI255993.1|BI255993 602976353F1 NIH_MGC_12 H... 394 e-107
 gi|12678524|gb|BG171821.1|BG171821 602322603F1 NIH_MGC_89 H... 393 e-106
 gi|10160188|gb|BE746196.1|BE746196 601578644F1 NIH_MGC_9 Ho... 391 e-106
 gi|12687397|gb|BG180694.1|BG180694 602329481F1 NIH_MGC_91 H... 373 e-100
 gi|13336094|gb|BG429588.1|BG429588 602501268F1 NIH_MGC_75 H... 371 e-100
 gi|8144363|gb|AW954680.1|AW954680 EST366750 MAGE resequence... 371 e-100
 gi|13999085|gb|BG719898.1|BG719898 602691430F1 NIH_MGC_97 H... 357 7e-96
 gi|11953928|gb|BF680033.1|BF680033 602154752F1 NIH_MGC_83 H... 357 7e-96
 gi|13972135|gb|BG701616.1|BG701616 602682503F1 NIH_MGC_95 H... 345 3e-92
 gi|10348906|gb|BE890514.1|BE890514 601431585F1 NIH_MGC_72 H... 345 3e-92
 gi|13969001|gb|BG700048.1|BG700048 602681055F1 NIH_MGC_95 H... 343 1e-91
 gi|9770617|gb|BE541972.1|BE541972 601064273F1 NIH_MGC_10 Ho... 331 4e-88

>gi|12848558|dbj|BAB27997.1| putative [Mus musculus]

EST Search:

Organ: eye
 Tissue type: retinoblastoma

Organ: ovary
 Tissue type: adenocarcinoma cell line

Organ: brain
 Tissue type: hippocampus

Organ: colon
 Tissue type: adenocarcinoma cell line

Human Sequences producing significant alignments: (bits) Value

gi|9124275|gb|BE253854.1|BE253854 601112818F1 NIH_MGC_16 Ho... 454 e-125
 gi|10156435|gb|BE742443.1|BE742443 601575210F1 NIH_MGC_9 Ho... 428 e-117
 gi|13967002|gb|BG699072.1|BG699072 602678713F1 NIH_MGC_95 H... 422 e-115
 gi|13401922|gb|BG469647.1|BG469647 602534103F1 NIH_MGC_15 H... 412 e-112
 gi|12604238|gb|BG110732.1|BG110732 602279029F1 NIH_MGC_86 H... 410 e-112
 gi|12609069|gb|BG115563.1|BG115563 602317253F1 NIH_MGC_88 H... 404 e-110
 gi|12761697|gb|BG251881.1|BG251881 602364502F1 NIH_MGC_90 H... 402 e-109
 gi|9186637|gb|BE302889.1|BE302889 ba70g10.y1 NIH_MGC_20 Hom... 398 e-108
 gi|14809963|gb|BI255993.1|BI255993 602976353F1 NIH_MGC_12 H... 394 e-107
 gi|10160188|gb|BE746196.1|BE746196 601578644F1 NIH_MGC_9 Ho... 391 e-106
 gi|12678524|gb|BG171821.1|BG171821 602322603F1 NIH_MGC_89 H... 385 e-104
 gi|8144363|gb|AW954680.1|AW954680 EST366750 MAGE resequence... 371 e-100
 gi|12687397|gb|BG180694.1|BG180694 602329481F1 NIH_MGC_91 H... 365 5e-98
 gi|13336094|gb|BG429588.1|BG429588 602501268F1 NIH_MGC_75 H... 363 2e-97
 gi|13999085|gb|BG719898.1|BG719898 602691430F1 NIH_MGC_97 H... 349 3e-93
 gi|11953928|gb|BF680033.1|BF680033 602154752F1 NIH_MGC_83 H... 349 3e-93
 gi|13972135|gb|BG701616.1|BG701616 602682503F1 NIH_MGC_95 H... 337 1e-89
 gi|10348906|gb|BE890514.1|BE890514 601431585F1 NIH_MGC_72 H... 337 1e-89
 gi|13969001|gb|BG700048.1|BG700048 602681055F1 NIH_MGC_95 H... 335 4e-89
 gi|14053553|gb|BG742900.1|BG742900 602632481F1 NCI_CGAP_Skn... 329 3e-87

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>gi|12850643|dbj|BAB28800.1| putative [Mus musculus]

EST Search:

Tissue type: T cells from T cell leukemia

Tissue type: T cells from T cell leukemia

Tissue type: placenta

Organ: brain

Tissue type: neuroblastoma

Organ: brain

Tissue type: neuroblastoma cells

Human Sequences producing significant alignments:

(bits) Value

gi 12903888 emb AL558907.1 AL558907 AL558907 LTI_NFL008_TC2... 613 e-173
gi 12900345 emb AL557084.1 AL557084 AL557084 LTI_FL012_TC1 ... 613 e-173
gi 12897788 emb AL555756.1 AL555756 AL555756 LTI_NFL006_PL2... 613 e-173
gi 13515355 gb BG519629.1 BG519629 602578744F1 NIH_MGC_19 H... 611 e-172
gi 12952470 emb AL583473.1 AL583473 AL583473 LTI_NFL004_NBC... 609 e-172
gi 12783279 emb AL519786.1 AL519786 AL519786 LTI_NFL004_NBC... 607 e-171
gi 13515189 gb BG519532.1 BG519532 602578613F1 NIH_MGC_19 H... 593 e-167
gi 12903886 emb AL558906.1 AL558906 AL558906 LTI_NFL008_TC2... 593 e-167
gi 12900344 emb AL557083.1 AL557083 AL557083 LTI_FL012_TC1 ... 593 e-167
gi 12790972 emb AL527479.1 AL527479 AL527479 LTI_NFL003_NBC... 583 e-164
gi 14177068 gb BG829481.1 BG829481 602763779F1 NIH_MGC_42 H... 571 e-160
gi 13583928 gb BG576275.1 BG576275 602595778F1 NIH_MGC_87 H... 565 e-158
gi 10157401 gb BE743409.1 BE743409 601573650F1 NIH_MGC_9 Ho... 565 e-158
gi 10161376 gb BE747384.1 BE747384 601580434F1 NIH_MGC_9 Ho... 561 e-157
gi 14177225 gb BG829638.1 BG829638 602763994F1 NIH_MGC_42 H... 557 e-156
gi 13980226 gb BG705661.1 BG705661 602668874F1 NIH_MGC_96 H... 543 e-152
gi 12786487 emb AL522994.1 AL522994 AL522994 LTI_NFL003_NBC... 541 e-151
gi 9806674 gb BE562954.1 BE562954 601336395F1 NIH_MGC_44 Ho... 539 e-151
gi 12340198 gb BF972983.1 BF972983 602241285F1 NIH_MGC_46 H... 537 e-150
gi 14060190 gb BG749537.1 BG749537 602707687F1 NIH_MGC_43 H... 535 e-150

>gi|12851759|dbj|BAB29156.1| putative [Mus musculus]

EST Search:

Organ: colon

Tissue type: adenocarcinoma cell line

Organ: pancreas

Tissue type: adenocarcinoma

Organ: lung

Tissue type: small cell carcinoma

Cell line: MGC3

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Organ: ovary
 Tissue type: fibrotheoma

Human Sequences producing significant alignments:	(bits)	Value
gi 13135151 gb BG328713.1 BG328713 602427988F1 NIH_MGC_15 H...	369	1e-99
gi 10149412 gb BE735420.1 BE735420 601304204F1 NIH_MGC_39 H...	365	2e-98
gi 9141043 gb BE267452.1 BE267452 601189745F2 NIH_MGC_7 Hom...	359	1e-96
gi 10984835 gb BF115433.1 BF115433 7n81h06.x1 NCI_CGAP_Ov18...	355	2e-95
gi 10700778 gb BF000503.1 BF000503 7h32a01.x1 NCI_CGAP_Co16...	345	2e-92
gi 6197433 gb AW149537.1 AW149537 xf39b12.x1 NCI_CGAP_Bm50...	341	3e-91
gi 14080921 gb BG770268.1 BG770268 602744858F1 NIH_MGC_49 H...	339	1e-90
gi 134111959 gb BG479680.1 BG479680 602527142F1 NIH_MGC_21 H...	339	1e-90
gi 10940810 gb BF111120.1 BF111120 7n43g10.x1 NCI_CGAP_Lu24...	337	5e-90
gi 9510747 gb BE464972.1 BE464972 hv76a11.x1 NCI_CGAP_Lu24 ...	335	2e-89
gi 13134589 gb BG328151.1 BG328151 602427216F1 NIH_MGC_15 H...	331	3e-88
gi 6710858 gb AW301181.1 AW301181 xs57d11.x1 NCI_CGAP_Kid11...	331	3e-88
gi 11450749 gb BF438232.1 BF438232 7q68g12.x1 NCI_CGAP_Lu24...	327	5e-87
gi 6709918 gb AW300318.1 AW300318 xs59g06.x1 NCI_CGAP_Kid11...	327	5e-87
gi 3056175 gb AA916783.1 AA916783 on10d05.s1 NCI_CGAP_Lu5 H...	325	2e-86
gi 9126816 gb BE256444.1 BE256444 601108430F1 NIH_MGC_16 Ho...	323	8e-86
gi 4985638 gb AI697738.1 AI697738 we16g07.x1 NCI_CGAP_Lu24 ...	321	3e-85
gi 3675611 gb AI147929.1 AI147929 qb38g05.x1 Soares_pregnant...	319	1e-84
gi 13705885 gb BG184198.1 BG184198 RST3119 Athersys RAGE Li...	313	8e-83
gi 9333920 gb BE388555.1 BE388555 601281843F1 NIH_MGC_44 Ho...	313	8e-83

>gi|12861668|dbj|BAB32258.1| putative [Mus musculus]

EST Search:

Tissue type: corresponding non cancerous liver tissue

Develop. stage: Adult

Organ: kidney

Organ: pancreas

Tissue type: epithelioid carcinoma cell line

Organ: testis

Organ: brain

Tissue type: hippocampus

Human Sequences producing significant alignments:	(bits)	Value
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gi 9875702 dbj AV654688.1 AV654688 AV654688 GLC Homo sapien...	168	2e-39
gi 7702359 gb AW770318.1 AW770318 h178e09.x1 NCI_CGAP_Kid13...	123	1e-25
gi 14178068 gb BG830481.1 BG830481 602767043F1 NIH_MGC_42 H...	121	5e-25
gi 13999085 gb BG719898.1 BG719898 602691430F1 NIH_MGC_97 H...	121	5e-25
gi 13967002 gb BG699072.1 BG699072 602678713F1 NIH_MGC_95 H...	121	5e-25
gi 12609069 gb BG115563.1 BG115563 602317253F1 NIH_MGC_88 H...	121	5e-25
gi 12604238 gb BG110732.1 BG110732 602279029F1 NIH_MGC_86 H...	121	5e-25
gi 9186637 gb BE302889.1 BE302889 ba70g10.y1 NIH_MGC_20 Hom...	121	5e-25
gi 8144363 gb AW954680.1 AW954680 EST366750 MAGE resequence...	121	5e-25
gi 1298897 gb W22050.1 W22050 61A4 Human retina cDNA Tsp509...	121	5e-25

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gi 10348906 gb BE890514.1 BE890514	601431585F1 NIH_MGC_72 H...	115	3e-23
gi 13336094 gb BG429588.1 BG429588	602501268F1 NIH_MGC_75 H...	113	1e-22
gi 13527202 gb BG535657.1 BG535657	602563366F1 NIH_MGC_77 H...	111	5e-22
gi 13523981 gb BG532442.1 BG532442	602561968F1 NIH_MGC_61 H...	111	5e-22
gi 1960040 gb AA307691.1 AA307691	EST178577 Colon carcinoma...	111	5e-22
gi 9186545 gb BE302797.1 BE302797	ba69a06.y1 NIH_MGC_20 Hom...	109	2e-21
gi 13972135 gb BG701616.1 BG701616	602682503F1 NIH_MGC_95 H...	107	8e-21
gi 13969001 gb BG700048.1 BG700048	602681055F1 NIH_MGC_95 H...	107	8e-21
gi 9770617 gb BE541972.1 BE541972	601064273F1 NIH_MGC_10 Ho...	107	8e-21
gi 13336068 gb BG429562.1 BG429562	602501238F1 NIH_MGC_75 H...	105	3e-20

>gi|14318640|gb|AAH09118.1|AAH09118 Unknown (protein for MGC:6971) [Mus musculus]

EST Search:

Organ: lung

Tissue type: carcinoid

Tissue type: Adrenal gland

Organ: liver

Tissue type: adenocarcinoma, cell line

Organ: lymph node

Tissue type: follicular lymphoma

Human Sequences producing significant alignments:	(bits)	Value
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gi 10940429 gb BF110739.1 BF110739	7n56b09.x1 NCI_CGAP_Lu24...	367	5e-99
gi 10721718 dbj AV704400.1 AV704400	AV704400 ADB Homo sapie...	341	3e-91
gi 12613045 gb BG119539.1 BG119539	602347238F1 NIH_MGC_90 H...	305	2e-80
gi 1472212 gb AA011185.1 AA011185	ze22d01.s1 Soares_fetal_h...	293	6e-77
gi 3838022 gb AI242625.1 AI242625	qu37c10.x1 NCI_CGAP_Lym5 ...	212	2e-52
gi 14166353 gb BG818766.1 BG818766	602779096F2 NCI_CGAP_Brn...	180	6e-43
gi 13708617 gb BG186930.1 BG186930	RST5907 Athersys RAGE Li...	153	1e-34
gi 4331367 gb AI469277.1 AI469277	tm07g05.x1 NCI_CGAP_Co14 ...	153	1e-34
gi 3677291 gb AI148822.1 AI148822	qc65e11.x1 Soares_placent...	153	1e-34
gi 3145479 gb AA969966.1 AA969966	op60e04.s1 Soares_NFL_T_G...	153	1e-34
gi 13707564 gb BG185877.1 BG185877	RST4830 Athersys RAGE Li...	151	6e-34
gi 10897098 gb BF091388.1 BF091388	CM0-TN0034-150900-551-e0...	145	3e-32
gi 5744726 gb AI952416.1 AI952416	wx73e03.x1 NCI_CGAP_Ov38 ...	145	3e-32
gi 8166900 gb AW975682.1 AW975682	EST387791 MAGE resequence...	127	8e-27
gi 3040766 gb AA905643.1 AA905643	oj97e05.s1 Soares_NFL_T_G...	127	8e-27
gi 14051179 gb BG740526.1 BG740526	602633034F1 NCI_CGAP_Skn...	115	3e-23
gi 12610022 gb BG116516.1 BG116516	602317614F1 NIH_MGC_88 H...	113	1e-22
gi 2767868 gb AA736634.1 AA736634	nw53d05.s1 NCI_CGAP_Ew1 H...	113	1e-22
gi 2752111 gb AA730907.1 AA730907	nw50c08.s1 NCI_CGAP_Ew1 H...	96	3e-17
gi 8015591 gb AW877247.1 AW877247	PM3-PT0039-010300-001-b06...	80	2e-12

>gi|13097495|gb|AAH03479.1|AAH03479 Unknown (protein for MGC:6908) [Mus musculus]

EST Search:

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Organ: skin
 Tissue type: melanotic melanoma, high MDR (cell line)

Organ: placenta

Organ: ovary
 Tissue type: adenocarcinoma cell line

Organ: lung
 Tissue type: small cell carcinoma

Human Sequences producing significant alignments:	(bits)	Value
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gi 14073190 gb BG762537.1 BG762537 602733994F1 NIH_MGC_49 H...	339	1e-90
gi 844959 gb R71442.1 R71442 yi51f01.r1 Soares placenta Nb2...	321	3e-85
gi 10156033 gb BE742041.1 BE742041 601594721F1 NIH_MGC_9 Ho...	313	8e-83
gi 10219393 gb BE798195.1 BE798195 601582662F1 NIH_MGC_7 Ho...	297	4e-78
gi 10216541 gb BE795343.1 BE795343 601586662F1 NIH_MGC_7 Ho...	297	4e-78
gi 10150854 gb BE736951.1 BE736951 601306912F1 NIH_MGC_39 H...	297	4e-78
gi 9331772 gb BE386407.1 BE386407 601273578F1 NIH_MGC_20 Ho...	297	4e-78
gi 1146469 gb N28234.1 N28234 EST51e15 WATM1 Homo sapiens c...	283	7e-74
gi 9334357 gb BE388992.1 BE388992 601284814F1 NIH_MGC_44 Ho...	281	3e-73
gi 9148949 gb BE274012.1 BE274012 601104628F1 NIH_MGC_14 Ho...	270	1e-69
gi 6926374 gb AW407317.1 AW407317 UI-HF-BL0-adj-e-12-0-Ui.r...	270	1e-69
gi 1383218 gb W73084.1 W73084 zd54a11.r1 Soares_fetal_heart...	268	4e-69
gi 9335068 gb BE389703.1 BE389703 601281945F1 NIH_MGC_44 Ho...	244	6e-62
gi 5674161 gb AI935291.1 AI935291 wp16e06.x1 NCI_CGAP_Lu19 ...	244	6e-62
gi 12678574 gb BG171871.1 BG171871 602322675F1 NIH_MGC_89 H...	238	4e-60
gi 5920966 gb AW055263.1 AW055263 wz16b09.x1 NCI_CGAP_Ut4 H...	236	1e-59
gi 1166345 gb N42314.1 N42314 yy06e04.r1 Soares_melanocyte ...	220	8e-55
gi 1319356 gb W37623.1 W37623 zc12d10.r1 Soares_parathyroid...	212	2e-52
gi 10265680 gb BE833302.1 BE833302 QV3-OT0065-280600-250-c0...	206	1e-50
gi 13409767 gb BG477488.1 BG477488 602521540F1 NIH_MGC_20 H...	202	2e-49

>gi|13278172|gb|AAH03930.1|AAH03930 RIKEN cDNA 1110029G07
 gene [Mus musculus]

EST Search:

Organ: skin
 Tissue type: melanotic melanoma

Organ: pancreas
 Tissue type: adenocarcinoma

Organ: brain
 Tissue type: hippocampus

Organ: ovary
 Tissue type: adenocarcinoma cell line

Human Sequences producing significant alignments:	(bits)	Value
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gi 10355896 gb BE893982.1 BE893982 601437772F1 NIH_MGC_72 H...	529	e-148
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gi|9759837|gb|BE531278.1|BE531278 601278395F1 NIH_MGC_39 Ho... 523 e-146
gi|13979738|gb|BG705419.1|BG705419 602685545F1 NIH_MGC_95 H... 519 e-145
gi|10157906|gb|BE743914.1|BE743914 601577970F1 NIH_MGC_9 Ho... 498 e-138
gi|9897009|gb|BE615410.1|BE615410 601280872F1 NIH_MGC_39 Ho... 468 e-129
gi|9896295|gb|BE614698.1|BE614698 601281684F1 NIH_MGC_39 Ho... 466 e-128
gi|13545873|gb|BG547208.1|BG547208 602574620F1 NIH_MGC_77 H... 436 e-120
gi|10320048|gb|BE871272.1|BE871272 601448967F1 NIH_MGC_65 H... 428 e-117
gi|10364365|gb|BE898169.1|BE898169 601431135F1 NIH_MGC_72 H... 412 e-112
gi|13671951|gb|BG620580.1|BG620580 602619745F1 NIH_MGC_79 H... 406 e-111
gi|13576308|gb|BG568655.1|BG568655 602587668F1 NIH_MGC_76 H... 391 e-106
gi|12340258|gb|BF973043.1|BF973043 602241361F1 NIH_MGC_46 H... 341 4e-91
gi|10084502|gb|BE697355.1|BE697355 QV1-CT0417-080800-299-a0... 333 9e-89
gi|9898221|gb|BE616622.1|BE616622 601278895F1 NIH_MGC_39 Ho... 329 1e-87
gi|2069938|gb|AA410814.1|AA410814 z36a05.r1 Soares ovary t... 297 5e-78
gi|2538826|gb|AA626439.1|AA626439 ab49g08.r1 Stratagene lun... 276 2e-71
gi|1049638|gb|H75695.1|H75695 yu07a04.r1 Soares fetal liver... 270 1e-69
gi|12397382|gb|BF991057.1|BF991057 CM1-GN0160-271000-502-a1... 266 2e-68
gi|992140|gb|H52299.1|H52299 yq81f07.r1 Soares fetal liver ... 264 7e-68
gi|1963274|gb|AA310946.1|AA310946 EST181721 Jurkat T-cells ... 262 3e-67

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>gi|12857745|dbj|BAB31099.1| putative [Mus musculus]

EST Search:

Organ: brain
Tissue type: neuroblastoma cells

Tissue type: mammary gland

Tissue type: placenta

Tissue type: ovary, tumor tissue

Human Sequences producing significant alignments:	(bits)	Value
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gi|12783826|emb|AL520333.1|AL520333 AL520333 LTI_NFL004_NBC... 835 0.0
gi|10936759|dbj|AU121524.1|AU121524 AU121524 MAMMA1 Homo sa... 831 0.0
gi|11000513|dbj|AU138992.1|AU138992 AU138992 PLACE1 Homo sa... 686 0.0
gi|10994408|dbj|AU133869.1|AU133869 AU133869 OVARC1 Homo sa... 654 0.0
gi|12893255|emb|AL553429.1|AL553429 AL553429 LTI_NFL006_PL2... 630 e-178
gi|13289457|gb|BG396009.1|BG396009 602458738F1 NIH_MGC_16 H... 628 e-177
gi|13999988|gb|BG720801.1|BG720801 602692025F1 NIH_MGC_97 H... 622 e-175
gi|13049086|gb|BG291280.1|BG291280 602388439F1 NIH_MGC_93 H... 609 e-171
gi|10936667|dbj|AU121432.1|AU121432 AU121432 MAMMA1 Homo sa... 567 e-159
gi|14063903|gb|BG753250.1|BG753250 602731650F1 NIH_MGC_43 H... 519 e-144
gi|10995473|dbj|AU134934.1|AU134934 AU134934 PLACE1 Homo sa... 511 e-142
gi|8278290|gb|BE018271.1|BE018271 bb77h08.y1 NIH_MGC_12 Hom... 498 e-138
gi|13994779|gb|BG715592.1|BG715592 602675925F1 NIH_MGC_96 H... 496 e-137
gi|9347181|gb|BE410731.1|BE410731 601301615F1 NIH_MGC_21 Ho... 492 e-136
gi|11285372|gb|BF338952.1|BF338952 602036022F1 NCI_CGAP_Brn... 428 e-117
gi|9873394|dbj|AV652380.1|AV652380 AV652380 GLC Homo sapien... 414 e-113
gi|1966540|gb|AA314211.1|AA314211 EST186056 Colon carcinoma... 408 e-111

gi|6922170|gb|AW403277.1|AW403277 UI-HF-BK0-abb-g-11-0-Ui.r... 379 e-102
gi|10293319|dbj|AV691456.1|AV691456 AV691456 GKC Homo sapien... 371 e-100

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gi|6896706|gb|AW392047.1|AW392047 QV4-ST0234-181199-037-c05... 363 2e-97

>gi|14789662|gb|AAH10758.1|AAH10758 Similar to carbonyl reductase 2 [Mus musculus]

EST Search:

Human Sequences producing significant alignments:	(bits)	Value
gi 14620169 gb BI160168.1 BI160168 602864026F1 NIH_MGC_42 H...	88	6e-15
gi 14320386 gb BG925863.1 BG925863 HNC21-1-B11.R HNC (Human...)	88	6e-15
gi 14178945 gb BG831358.1 BG831358 602766220F1 NIH_MGC_42 H...	88	6e-15
gi 14177680 gb BG830093.1 BG830093 602764845F1 NIH_MGC_42 H...	88	6e-15
gi 14058983 gb BG748330.1 BG748330 602706579F1 NIH_MGC_43 H...	88	6e-15
gi 14058856 gb BG748203.1 BG748203 602705827F1 NIH_MGC_43 H...	88	6e-15
gi 13982131 gb BG706614.1 BG706614 602674104F1 NIH_MGC_96 H...	88	6e-15
gi 13413874 gb BG481595.1 BG481595 602528316F1 NIH_MGC_21 H...	88	6e-15
gi 13404430 gb BG472244.1 BG472244 602513756F1 NIH_MGC_16 H...	88	6e-15
gi 13340715 gb BG434209.1 BG434209 602506154F1 NIH_MGC_79 H...	88	6e-15
gi 13137575 gb BG331137.1 BG331137 602431839F1 NIH_MGC_18 H...	88	6e-15
gi 13032709 gb BG283133.1 BG283133 602406785F1 NIH_MGC_91 H...	88	6e-15
gi 12683322 gb BG176619.1 BG176619 602313206F1 NIH_MGC_85 H...	88	6e-15
gi 12615652 gb BG122143.1 BG122143 602349585F1 NIH_MGC_90 H...	88	6e-15
gi 12412330 gb BG025585.1 BG025585 602274505F1 NIH_MGC_85 H...	88	6e-15
gi 12343809 gb BF976594.1 BF976594 602244271F1 NIH_MGC_48 H...	88	6e-15
gi 12342418 gb BF975203.1 BF975203 602244705F1 NIH_MGC_48 H...	88	6e-15
gi 11970704 gb BF685296.1 BF685296 602141648F1 NIH_MGC_46 H...	88	6e-15
gi 11949082 gb BF675187.1 BF675187 602138110F1 NIH_MGC_83 H...	88	6e-15
gi 11641972 gb BF568592.1 BF568592 602184218F1 NIH_MGC_42 H...	88	6e-15
gi 11617689 gb BF530338.1 BF530338 602071618F1 NCI_CGAP_Brn...	88	6e-15
gi 11263622 gb BF315274.1 BF315274 601902672F1 NIH_MGC_19 H...	88	6e-15
gi 11258150 gb BF310575.1 BF310575 601895295F2 NIH_MGC_19 H...	88	6e-15
gi 11252161 gb BF305282.1 BF305282 601892747F1 NIH_MGC_17 H...	88	6e-15

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gi|11251336|gb|BF304588.1|BF304588 601887980F1 NIH_MGC_17 H... 88 6e-15
gi|11151599|gb|BF237681.1|BF237681 601841865F1 NIH_MGC_46 H... 88 6e-15
gi|11098442|gb|BF204856.1|BF204856 601867158F1 NIH_MGC_17 H... 88 6e-15
gi|11098117|gb|BF204531.1|BF204531 601868138F1 NIH_MGC_17 H... 88 6e-15
gi|10726004|dbj|AV708739.1|AV708739 AV708739 ADC Homo sapie... 88 6e-15
gi|10404479|gb|BE909167.1|BE909167 601501782F1 NIH_MGC_70 H... 88 6e-15
gi|10390490|gb|BE901372.1|BE901372 601674675F1 NIH_MGC_21 H... 88 6e-15
gi|10346623|gb|BE889373.1|BE889373 601513264F1 NIH_MGC_71 H... 88 6e-15
gi|10297085|dbj|AV695222.1|AV695222 AV695222 GKC Homo sapie... 88 6e-15
gi|10296576|dbj|AV694713.1|AV694713 AV694713 GKC Homo sapie... 88 6e-15
gi|10296182|dbj|AV694319.1|AV694319 AV694319 GKC Homo sapie... 88 6e-15
gi|10293455|dbj|AV691592.1|AV691592 AV691592 GKC Homo sapie... 88 6e-15
gi|10216172|gb|BE794974.1|BE794974 601589746F1 NIH_MGC_7 Ho... 88 6e-15
gi|9882981|dbj|AV661967.1|AV661967 AV661967 GLC Homo sapien... 88 6e-15
gi|9882826|dbj|AV661812.1|AV661812 AV661812 GLC Homo sapien... 88 6e-15
gi|9875231|dbj|AV654217.1|AV654217 AV654217 GLC Homo sapien... 88 6e-15
gi|9874551|dbj|AV653537.1|AV653537 AV653537 GLC Homo sapien... 88 6e-15
gi|9874547|dbj|AV653533.1|AV653533 AV653533 GLC Homo sapien... 88 6e-15
gi|9156256|gb|BE281240.1|BE281240 601155341F1 NIH_MGC_21 Ho... 88 6e-15
gi|9137978|gb|BE264422.1|BE264422 601191730F1 NIH_MGC_7 Hom... 88 6e-15
gi|9137251|gb|BE263706.1|BE263706 601192146F1 NIH_MGC_7 Hom... 88 6e-15
gi|9133208|gb|BE313377.1|BE313377 601147921F1 NIH_MGC_19 Ho... 88 6e-15
gi|8750451|gb|BE207053.1|BE207053 ba09d08.y1 NIH_MGC_7 Homo... 88 6e-15
gi|8147585|gb|AW957902.1|AW957902 EST369972 MAGE resequence... 88 6e-15
gi|8147508|gb|AW957825.1|AW957825 EST369895 MAGE resequence... 88 6e-15
gi|6588561|gb|AW245568.1|AW245568 2822726.5prime NIH_MGC_7 ... 88 6e-15
gi|2537901|gb|AA625514.1|AA625514 af72e06.r1 Soares_NhHMPu... 88 6e-15
gi|2159374|gb|AA446709.1|AA446709 zw84d08.r1 Soares_total_f... 88 6e-15
gi|2112928|gb|AA429728.1|AA429728 zv60c08.r1 Soares_testis... 88 6e-15
gi|2111979|gb|AA430753.1|AA430753 zw52g09.r1 Soares_total_f... 88 6e-15
gi|1272012|gb|W00611.1|W00611 yy71a11.r1 Soares_multiple_sc... 88 6e-15
gi|1271974|gb|W00555.1|W00555 yy70g11.r1 Soares_multiple_sc... 88 6e-15
gi|1087367|gb|H91789.1|H91789 yv04c07.r1 Soares fetal liver... 88 6e-15
gi|1063794|gb|H84670.1|H84670 ys66c06.r1 Soares retina N2b4... 88 6e-15
gi|1044285|gb|H72469.1|H72469 ys07a02.r1 Soares fetal liver... 88 6e-15
gi|1023609|gb|H64869.1|H64869 yr68e02.r1 Soares fetal liver... 88 6e-15
gi|663547|gb|T60510.1|T60510 yb86c11.r1 Stratagene liver (#... 88 6e-15
gi|13976241|gb|BG703674.1|BG703674 602686647F1 NIH_MGC_95 H... 84 1e-13
gi|14568476|gb|BI117575.1|BI117575 602866754F1 NIH_MGC_7 Ho... 82 4e-13
gi|9155643|gb|BE280635.1|BE280635 601155778F1 NIH_MGC_21 Ho... 82 4e-13

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gi|1046607|gb|H73548.1|H73548 ys10h05.r1 Soares fetal liver... 80 2e-12
gi|11154540|gb|BF240616.1|BF240616 601875744F1 NIH_MGC_55 H... 78 6e-
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Table 3: Bacterial SDRs derived from non-redundant NCBI Database

>gi|13701031|dbj|BAB42326.1| 3-oxoacyl- reductase [Staphylococcus aureus subsp. aureus N315]

>gi|3170581|gb|AAC18111.1| ketoreductase [Streptomyces roseofulvus]

>gi|2226002|emb|CAA74371.1| glucose-1-dehydrogenase [Staphylococcus xylosus]

>gi|4240408|gb|AAD13539.1| reductase homolog [Streptomyces cyanogenus]

>gi|14521852|ref|NP_127328.1| 3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [Pyrococcus abyssi]

>gi|9789233|gb|AAF98275.1|AF197933_5 beta-ketoacyl-ACP reductase [Streptococcus pneumoniae]

>gi|9967599|emb|CAC05675.1| putative keto reductase [Streptomyces antibioticus]

>gi|12513057|gb|AAG54602.1|AE005204_12 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12513383|gb|AAG54850.1|AE005230_10 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12720847|gb|AAK02663.1| YdfG [Pasteurella multocida]

>gi|12744823|gb|AAK06787.1|AF324838_6 putative ketoreductase SimA6 [Streptomyces antibioticus]

>gi|13622804|gb|AAK34493.1| putative beta-ketoacyl-ACP reductase [Streptococcus pyogenes M1 GAS]

>gi|14280346|gb|AAK57528.1| polyketide ketoreductase PgaD [Streptomyces sp. PGA64]

>gi|14346021|gb|AAK60002.1| ketoreductase-like protein [Streptomyces aureofaciens]

>gi|14346023|gb|AAK60004.1| oxygenase-like protein [Streptomyces aureofaciens]

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>gi|14486276|gb|AAK61717.1| ketoreductase-like protein [Streptomyces aureofaciens]

>gi|294354|gb|AAA16128.1| The first start codon in the ORF is found at position 2466 [Pseudomonas sp.]

>gi|1502421|gb|AAC44307.1| 3-ketoacyl-acyl carrier protein reductase

>gi|4160474|gb|AAD05259.1| 3-ketoacyl-CoA reductase PhaB [Bacillus megaterium]

>gi|4416467|gb|AAD20367.1| dehydrogenase dhgA [Mycobacterium avium]

>gi|4886772|gb|AAD32035.1|AF093787_3 CylG [Streptococcus agalactiae]

>gi|14520705|ref|NP_126180.1| OXIDOREDUCTASE [Pyrococcus abyssi]

>gi|5669916|gb|AAD46515.1|AF145724_4 oxidoreductase homolog [Streptomyces albus]

>gi|6018300|gb|AAF01806.1|AF187532_2 C-7 ketoreductase [Streptomyces nogalater]

>gi|8896110|gb|AAF81238.1| putative beta-ketoacyl reductase [Streptomyces griseus subsp. griseus]

>gi|11354347|pir||F82128 3-oxoacyl-(acyl-carrier-protein) reductase VC2021 [imported] - Vibrio cholerae (group O1 strain N16961)

>gi|9944997|gb|AAG03070.1|AF293355_6 putative bifunctional cyclase/reductase [Streptomyces collinus]

>gi|9944998|gb|AAG03071.1|AF293355_7 putative reductase [Streptomyces collinus]

>gi|10174123|dbj|BAB05225.1| oxidoreductase [Bacillus halodurans]

>gi|11036625|gb|AAG01883.1| ribitol dehydrogenase [Escherichia coli]

>gi|12382035|dbj|BAB20935.2| ORF [Staphylococcus aureus]

>gi|12514413|gb|AAG55660.1|AE005304_5 putative fatty acyl chain reductase [Escherichia coli O157:H7 EDL933]

>gi|12514637|gb|AAG55839.1|AE005319_8 3-oxoacyl-[acyl-carrier-protein]

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>gi|12515117|gb|AAG56223.1|AE005351_2 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12515526|gb|AAG56544.1|AE005380_3 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12517239|gb|AAG57883.1|AE005505_1 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12656392|gb|AAK00851.1|AF298896_1 hypothetical protein [Burkholderia pseudomallei]

>gi|12721234|gb|AAK03000.1| unknown [Pasteurella multocida]

>gi|12722349|gb|AAK04000.1| FabG [Pasteurella multocida]

>gi|12744826|gb|AAK06790.1|AF324838_9 putative reductase SimA9 [Streptomyces antibioticus]

>gi|13507282|gb|AAK28547.1| putative oxidoreductase [Yersinia pseudotuberculosis]

>gi|13621828|gb|AAK33602.1| putative 5-keto-D-gluconate 5-reductase [Streptococcus pyogenes M1 GAS]

>gi|13702422|dbj|BAB43563.1| ORFID:SA2260~hypothetical protein, similar to glucose 1-dehydrogenase [Staphylococcus aureus subsp. aureus N315]

>gi|2337820|emb|CAA74250.1| putative FabG protein [Bacillus subtilis]

>gi|11356556|pir|T44878 3-oxoacyl-[acyl-carrier protein] reductase homolog [imported] - Mycobacterium leprae

>gi|11890400|gb|AAG41118.1|AF080431_1 putative blue fluorescent protein [Vibrio vulnificus]

>gi|12514398|gb|AAG55648.1|AE005303_4 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12516801|gb|AAG57544.1|AE005472_11 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|12518153|gb|AAG58600.1|AE005571_17 putative beta-ketoacyl-ACP reductase [Escherichia coli O157:H7 EDL933]

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>gi|12519258|gb|AAG59448.1|AE005657_8 putative oxidoreductase [Escherichia coli O157:H7 EDL933]

>gi|13621671|gb|AAK33459.1| putative dehydrogenase / oxidoreductase [Streptococcus pyogenes M1 GAS]

>gi|13622089|gb|AAK33840.1| putative oxidoreductase [Streptococcus pyogenes M1 GAS]

>gi|13700042|dbj|BAB41341.1| acetoinreductase [Staphylococcus aureus subsp. aureus N315]

>gi|13702428|dbj|BAB43569.1| ORFID:SA2266~hypothetical protein, similar to oxidoreductase [Staphylococcus aureus subsp. aureus N315]

>gi|13883461|gb|AAK47965.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Mycobacterium tuberculosis CDC1551]

Formularende

>gi|13622804|gb|AAK34493.1| putative beta-ketoacyl-ACP reductase [Streptococcus pyogenes M1 GAS]

Formularende

>gi|12054781|emb|CAC20627.1| hypothetical protein [Listeria monocytogenes]

>gi|1742522|dbj|BAA15229.1| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase). [Escherichia coli]

>gi|11353996|pir||F81902 probable oxidoreductase NMA1336 [imported] - Neisseria meningitidis (group A strain Z2491)

>gi|6715317|gb|AAF26372.1|AF204735_4 putative NADP-dependent oxidoreductase [Streptomyces coelicolor A3(2)]

>gi|7471791|pir||C75365 daunorubicin C-13 ketoreductase - Deinococcus radiodurans (strain R1)

>gi|146280|gb|AAC13413.1| glucitol-6-phosphate dehydrogenase (gutD) [Escherichia coli]

>gi|5688848|dbj|BAA82699.1| Orf2 [Streptomyces coelicolor]

>gi|2842819|gb|AAC38850.1| pteridine reductase [Trypanosoma cruzi]

>gi|13701301|dbj|BAB42595.1| ORFID:SA1333~hypothetical protein, similar to oxidoreductase [Staphylococcus aureus subsp. aureus N315]

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>gi|11356654|pir||T44745 probable oxidoreductase [imported] - *Mycobacterium leprae*

>gi|6562733|emb|CAB62872.1| conserved hypothetical protein, MAL4P2.31 [Plasmodium falciparum]

>gi|11355853|pir||C82155 probable C-factor VC1815 [imported] - *Vibrio cholerae* (group O1 strain N16961)

>gi|14587405|dbj|BAB61742.1| cyclohexanol dehydrogenase [Acinetobacter sp. NCIMB9871]

>gi|14600158|gb|AAK71281.1|AF387640_27 keto acyl carrier protein reductase [Coxiella burnetii]

>gi|14245893|dbj|BAB56288.1| acetoin(diacetyl)reductase [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14247001|dbj|BAB57393.1| 3-oxoacyl-(acyl-carrier protein) reductase [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14247273|dbj|BAB57664.1| hypothetical protein [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14248102|dbj|BAB58490.1| hypothetical protein [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14248246|dbj|BAB58634.1| hypothetical protein [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14248252|dbj|BAB58640.1| hypothetical protein [*Staphylococcus aureus* subsp. *aureus* Mu50]

>gi|14280348|gb|AAK57530.1| oxygenase-reductase PgaM [Streptomyces sp. PGA64]

>gi|14289341|gb|AAK58906.1|AF279141_4 cis-diol dehydrogenase [Rhodococcus sp. 19070]

>gi|14324288|dbj|BAB59216.1| glucose 1-dehydrogenase [Thermoplasma volcanium]

>gi|14325607|dbj|BAB60510.1| 3-oxoacyl-acyl carrier protein reductase [Thermoplasma volcanium]

>gi|14325671|dbj|BAB60574.1| glucose 1-dehydrogenase [Thermoplasma volcanium]

>gi|14349112|emb|CAC41336.1| acetoacetyl-CoA reductase [Azotobacter sp. FA8]

>gi|14423345|gb|AAK62355.1|AF380367_5 DbtB [Burkholderia sp. DBT1]

>gi|14518347|ref|NP_116830.1| MS142, putative gluconate dehydrogenase [Microscilla sp. PRE1]

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>gi|14523094|gb|AAK64694.1| putative [Sinorhizobium meliloti]
>gi|14523350|gb|AAK64928.1| IdnO1 gluconate 5-dehydrogenase [Sinorhizobium meliloti]
>gi|14523471|gb|AAK65040.1| putative [Sinorhizobium meliloti]
>gi|14523623|gb|AAK65178.1| probable [Sinorhizobium meliloti]

>gi|38683|emb|CAA37101.1| nodG protein (AA 1-254) [Azospirillum brasilense]

>gi|487893|gb|AAA19620.1| ORF5
>gi|510725|gb|AAB36565.1| ketoreductase [Streptomyces venezuelae]

>gi|12824504|gb|AAE49410.1| Sequence 2 from patent US 6110704

>gi|1828502|gb|AAB42956.1| Sequence 5 from patent US 5573915
>gi|3010372|gb|AAC10978.1|I74231 Sequence 13 from patent US 5686590

>gi|9928758|emb|CAC05159.1| SEQ ID NO 46F [Mycobacterium tuberculosis]

>gi|13443714|emb|CAC34889.1| ORF16; 3,4-Reduktase [Saccharopolyspora spinosa]

>gi|12542824|emb|CAC25795.1| RXA02474 [Corynebacterium glutamicum]
>gi|12542826|emb|CAC25796.1| RXA02453 [Corynebacterium glutamicum]

>gi|12542872|emb|CAC25819.1| RXA00825 [Corynebacterium glutamicum]

>gi|12542900|emb|CAC25833.1| RXA00251 [Corynebacterium glutamicum]

>gi|12542902|emb|CAC25834.1| RXN02654 [Corynebacterium glutamicum]

>gi|12544154|emb|CAC26450.1| RXA01764 [Corynebacterium glutamicum]

>gi|12544216|emb|CAC26481.1| RXA00681 [Corynebacterium glutamicum]

>gi|12544300|emb|CAC26523.1| RXN01090 [Corynebacterium glutamicum]
>gi|10050763|gb|AAE27670.1| Sequence 2 from patent US 5955319

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>gi|10280064|emb|CAC09972.1| Glucose-Degydrogenase aus *Bacillus megaterium*

>gi|6741907|emb|CAB69606.1| unnamed protein product [unidentified]

>gi|6741907|emb|CAB69606.1| unnamed protein product [unidentified]

>gi|6740927|emb|CAB69495.1| CONIFERYLALKOHOL-DEHYDROGENASE [unidentified]

>gi|1247706|emb|CAA01852.1| CoA reductase [*Allochromatium vinosum*]

>gi|345143|emb|CAA00174.1| glucose dehydrogenase [*Bacillus megaterium*]

>gi|532243|gb|AAA65204.1| daunorubicin-doxorubicin polyketide synthase

>gi|13702128|dbj|BAB43420.1| ORFID:SA2119~hypothetical protein, similar to dehydrogenase [*Staphylococcus aureus* subsp. *aureus* N315]

>gi|13622711|gb|AAK34408.1| putative oxidoreductase [*Streptococcus pyogenes* M1 GAS]

>gi|12514413|gb|AAG55660.1|AE005304_5 putative fatty acyl chain reductase [*Escherichia coli* O157:H7 EDL933]

>gi|15026474|gb|AAK81319.1|AE007836_1 Possible S-layer protein [*Clostridium acetobutylicum*]

>gi|15026554|gb|AAK81391.1|AE007844_1 3-oxoacyl-acyl carrier protein reductase [*Clostridium acetobutylicum*]

>gi|15026670|gb|AAK81497.1|AE007854_4 3-ketoacyl-acyl carrier protein reductase [*Clostridium acetobutylicum*]

>gi|15004706|ref|NP_149166.1| Oxidoreductase [*Clostridium acetobutylicum*]

>gi|15004755|ref|NP_149215.1| Oxidoreductase [*Clostridium acetobutylicum*]

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Table 4: FabG SDR Proteins derived from non redundant NCBI Database

- >gi|14782791|ref|XP_042583.1|FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, *E coli*) like [Homo sapiens]
- >gi|13701031|dbj|BAB42326.1|3-oxoacyl- reductase [*Staphylococcus aureus* subsp. *aureus* N315]
- >gi|13622804|gb|AAK34493.1|putative beta-ketoacyl-ACP reductase [*Streptococcus pyogenes* M1 GAS]
- >gi|14247001|dbj|BAB57393.1|3-oxoacyl-(acyl-carrier protein) reductase [*Staphylococcus aureus* subsp. *aureus* Mu50]
- >gi|14041700|emb|CAC38444.1|DJ1033B10.9.1 (FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, *E coli*) like, isoform 1) [Homo sapiens]
- >gi|14041699|emb|CAC38443.1| DJ1033B10.9.2 (FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, *E coli*) like, isoform 2) [Homo sapiens]
- >gi|12514637|gb|AAG55839.1|AE005319 8 3-oxoacyl-[acyl-carrier-protein] reductase [*Escherichia coli* O157:H7 EDL933]
- >gi|13360935|dbj|BAB34894.1|3-oxoacyl-[acyl-carrier-protein] reductase [*Escherichia coli* O157:H7]
- >gi|12722349|gb|AAK04000.1|FabG [*Pasteurella multocida*]
- >gi|12824504|gb|AAE49410.1| Sequence 2 from patent US 6110704
- >gi|10580854|gb|AAC19676.1|3-oxoacyl-[acyl-carrier-protein] reductase; FabG [*Halobacterium* sp. NRC-1]
- >gi|10175111|dbj|BAB06210.1|3-oxoacyl-(acyl-carrier protein) reductase [*Bacillus halodurans*]
- >gi|8978670|dbj|BAA98506.1|oxoacyl (carrier protein) reductase [*Chlamydophila pneumoniae* J138]
- >gi|4376571|gb|AAD18445.1|Oxoacyl (Carrier Protein) Reductase [*Chlamydophila pneumoniae* CWL029]
- >gi|1787335|gb|AAC74177.1|3-oxoacyl-[acyl-carrier-protein] reductase [*Escherichia coli* K12]
- >gi|3328647|gb|AAC67830.1|Oxoacyl (Carrier Protein) Reductase [*Chlamydia trachomatis*]
- >gi|10639611|emb|CAC11583.1|3-oxoacyl-[acyl-carrier-protein] reductase related protein [*Thermoplasma acidophilum*]
- >gi|10639394|emb|CAC11396.1|3-ketoacyl-acyl carrier protein reductase related protein [*Thermoplasma acidophilum*]

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- >gi|10039021|dbj|BAB13055.1|3-oxoacyl-[acyl-carrier protein] reductase [Buchnera sp. APS]
- >gi|9949065|gb|AAC06355.1|AE004722_11 3-oxoacyl-[acyl-carrier-protein [Pseudomonas aeruginosa]
- >gi|9789233|gb|AAF98275.1|AF197933_5 beta-ketoacyl-ACP reductase [Streptococcus pneumoniae]
- >gi|5459072|emb|CAB50558.1|3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [Pyrococcus abyssi]
- >gi|2738155|gb|AAB94395.1|3-oxoacyl-acyl carrier protein reductase [Pseudomonas aeruginosa]
- >gi|1651536|dbj|BAA35901.1|3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100). [Escherichia coli]
- >gi|3861291|emb|CAA15190.1|3-OXOACYL REDUCTASE (fabG) [Rickettsia prowazekii]
- >gi|1561753|gb|AAC69638.1|3-ketoacyl reductase [Mycobacterium smegmatis]
- >gi|2183267|gb|AAC46203.1|ketoacyl-reductase [Mycobacterium avium]
- >gi|1502421|gb|AAC44307.1|3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]
- >gi|1173841|gb|AAC43589.1|3-ketoacyl-ACP reductase [Vibrio harveyi]
- >gi|3282804|gb|AAC38650.1|3-oxoacyl-acyl carrier protein reductase [Salmonella typhimurium]
- >gi|2253068|emb|CAB10712.1|hypothetical protein Rv2129c [Mycobacterium tuberculosis]
- >gi|1573112|gb|AAC21824.1|3-ketoacyl-acyl carrier protein reductase (fabG) [Haemophilus influenzae Rd]
- >gi|2337820|emb|CAA74250.1|putative FabG protein [Bacillus subtilis]
- >gi|2633963|emb|CAB13464.1|3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]
- >gi|1651214|dbj|BAA13560.1|beta-ketoacyl-ACP reductase [Actinobacillus actinomycetemcomitans]
- >gi|145881|gb|AAA23739.1|biotin carboxylase [Escherichia coli]
- >gi|2313678|gb|AAD07627.1|3-ketoacyl-acyl carrier protein reductase (fabG) [Helicobacter pylori 26695]

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>gi|4155047|gb|AAD06084.1|ACETYL-COENZYME A CARBOXYLASE SUBUNIT
A [Helicobacter pylori J99]

>gi|6045047|dbj|BAA85256.1|3-oxoacyl-[acyl carrier protein] reductase
homolog [Moritella marina]

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Table 5: SDRs in Fungi derived from non redundant NCB Database

- >gi|5689604|emb|CAB51900.1| 1,3,6,8-tetrahydroxynaphthalene reductase [Aspergillus fumigatus]
- >gi|13570027|gb|AAG29497.2|AF290182_1 tetrahydroxynaphthalene reductase [Magnaporthe grisea]
- >gi|1592833|gb|AAB42156.1| ketoreductase [Aspergillus parasiticus]
- >gi|431103|gb|AAA19514.1| polyhydroxynaphthalene reductase [Magnaporthe grisea]
- >gi|3425989|dbj|BAA32378.1| Brn1 [Curvularia intermedia]
- >gi|450261|gb|AAA53572.1| verA [Emericella nidulans]
- >gi|12718334|emb|CAC28569.1| conserved hypothetical protein [Neurospora crassa]
- >gi|11359360|pir||T51084 3-oxoacyl-[acyl-carrier-protein]-reductase (oar-1) [imported] - Neurospora crassa
- >gi|4499846|emb|CAB39316.1| oxidoreductase [Claviceps purpurea]
- >gi|1902911|dbj|BAA18962.1| reductase [Colletotrichum lagenarium]

Claims

1. A method for identifying or verifying members of the short chain
5 dehydrogenase (SDR) family comprising the steps

- (a) providing a target sequence of molecules to be classified,
- (b) comparing said target sequence with core SDR motifs selected from
 - (i) MV1 being derived from the motif MT1:TGxxxGxG by replacement of 0 to 2 amino acids,
 - (ii) MT2:NN(0-2:x)AG,
 - (iii) MT3:N, located at a position 90-110 relative to MT1,
 - (iv) MV4 being derived from the motif MT4:S(11-52:x)YxxxK by replacement of 0-2 amino acids and
 - (v) MT5:PG,
- (c) determining positive SDR candidates containing
 - (i) at least the core SDR motifs MV1 and MV4 and
 - (ii) at least 7 of the 14 amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5 and
- (d) classifying positive SDR candidates as belonging to the SDR family.

2. The method according to claim 1 further comprising a step

- (e) ranking of the positive SDR candidates obtained according to the number of amino acids matching with motifs MT1, MT2, MT3, MT4 and MT5.

3. The method according to claim 1 or 2, wherein in step (b) the target sequence is compared with core SDR motifs selected from

- (i) MT1:TGxxxGxG,
- (ii) MT2:NN(0-2:x)AG,
- (iii) MT3:N, located at position 90-110 relative to MT1,
- (iv) MT4:S(11-52:x)YxxxK and
- (v) MT5:PG, and

in step (c) positive SDR candidates are determined containing

- (i) at least the core SDR motifs MT1 and MT4 and

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- (ii) at least 7 of the 14 amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5.
4. The method according to any of claims 1-3, wherein in step (c) positive SDR candidates are determined containing
- (i) at least the core SDR motifs MV1, MV4 and one of MT2, MT3 and MT5 and
 - (ii) at least 7 of the 14 amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5.
5. The method according to any of claims 1-4, wherein in step (c) positive SDR candidates are determined containing
- (i) the core SDR motifs MV1, MV4, MT2, and MT3 or MV1, MV4, MT2 and MT5 or MV1, MV4, MT3 and MT5.
10. The method according to any of claims 1-5, wherein positive SDR candidates are determined containing the core SDR motifs MV1, MV4, MT2, MT3 and MT5.
15. The method according to claim 1, wherein in step (c) positive candidates are determined containing at least 9, preferably at least 11 of the 14 amino acids contained in the motifs MT1, MT2, MT3, MT4 and MT5.
20. The method according to any of the preceding claims, wherein MT2 is defined as NNAG.
25. The method according to any of the preceding claims, wherein MV4 is derived from the motif MT'4:S(11-52:x)YxASK by replacement of 0-2 amino acids.
30. The method according to claim 9, wherein in step (c) positive candidates are determined containing at least 9, preferably at least 11, particular preferably at least 13 of the 16 amino acids contained in the core motifs used.
- 35.

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11. The method according to any of the preceding claims, wherein MT₂ and/or MT₅ are extended for identifying or verifying FabG_SDRs, wherein MT_y2:VxVNNAG, wherein V can be replaced and MT_y5:PGFI, wherein F and/or I are used as search motif.
12. The method according to any of the preceding claims further comprising one or more of the following further steps:
 - (i) three-dimensional structure comparison and
 - (ii) biological function analysis.
13. Member of the short-chain dehydrogenase (SDR) family identified with the method according to any of claims 1-12.
14. SDR according to claim 13, wherein it is selected from the SDRs shown in Tables 1-5.
15. A method for providing modulators for members of the short chain dehydrogenase (SDR) family comprising the steps
 - (a) providing one or more target sequences of members of the short chain dehydrogenase family based on an algorithm using core SDR motifs for searching members of the SDR family and
 - (b) providing modulators, which enhance or inhibit the activity of the members of the short chain dehydrogenase family.
16. The method according to claim 15, wherein in step (a) the method according to any of claims 1-12 is applied.
17. The method according to claim 15 or 16, wherein in step (b) a protein sequence alignment with known SDR sequences is performed for pre-selecting possible modulators.
18. A method for evaluation of lead-candidates for possible modulators of a member of the SDR family comprising the steps
 - (a) providing one or more target sequences of members of the short chain dehydrogenase family based on an algorithm using core SDR motifs for searching members of the SDR family,

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- (b) ranking the target sequences according to the number of amino acids matching with the core SDR motifs used and
- (c) deriving lead-candidates from metabolites of evolutionary related SDR enzymes.

5

19. The method according to claim 18, wherein in step (a) the method according to any of claims 1-12 is applied.

20. A method for providing a pharmaceutical agent comprising the steps

- (a) providing one or more target sequences of members of the short chain dehydrogenase family based on an algorithm using core SDR motifs for searching members of the SDR family,
- (b) providing modulators, which enhance or inhibit the activity of the members of the short chain dehydrogenase family and
- (c) formulating said modulators as pharmaceutical agent.

21. The method according to claim 20, wherein in step (a) the method according to claims 1-12 is applied.

20

22. The method according to claim 20 or 21, wherein in step (b) the method according to any of claims 15-17 is applied.

23. The method according to any of claims 20-22, wherein a modulator is provided, which enhances the activity of the members of the short chain dehydrogenase family.

24. The method according to any of claims 20-22, wherein a modulator is provided, which inhibits the activity of the members of the short chain dehydrogenase family.

30
35 25. The method according to any of claims 20-24, wherein the validation of a modulator or a function of a SDR enzyme found with an algorithm using core SDR motifs is performed with biochemical methods.

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26. The method according to any of claims 20-29, wherein expressed sequence tags and gene sequence comparison are used to provide a function of the member of the short chain dehydrogenase family, which has been identified or verified with an algorithm using core SDR motifs.
5
27. The method according to any of claims 20-26, wherein a modulator or a function of an SDR enzyme found with an algorithm using core SDR motifs is validated high throughput function screening for function identification, UHTS for lead compounds, molecular homology modelling, substrate docking simulations, tissue expression, cDNA arrays or analysis of disease in animal or in vitro model systems.
10
28. The method according to any of claims 20-27, wherein a human SDR enzyme is provided and the pharmaceutical agent is applied for therapeutical or diagnostical purposes.
15
29. The method according to claim 28, wherein the human SDR enzyme is selected from the human SDRs shown in Table 1 or 2.
20
30. The method according to any of claims 20-28, wherein an SDR from a pathogen or/and a fungi is provided to obtain a high specific pharmaceutical agent.
25
31. The method according to claim 30, wherein the SDR is selected from the SDRs shown in Table 3, 4 or 5.
32. The method according to claims 20-31, wherein an SDR enzyme with high homology is provided, which constitutes an essential enzyme.
30
33. The method according to any of claims 20-31, wherein a SDR enzyme with low homology or high divergence between different species is provided, which allows for a species specific modulation.
35

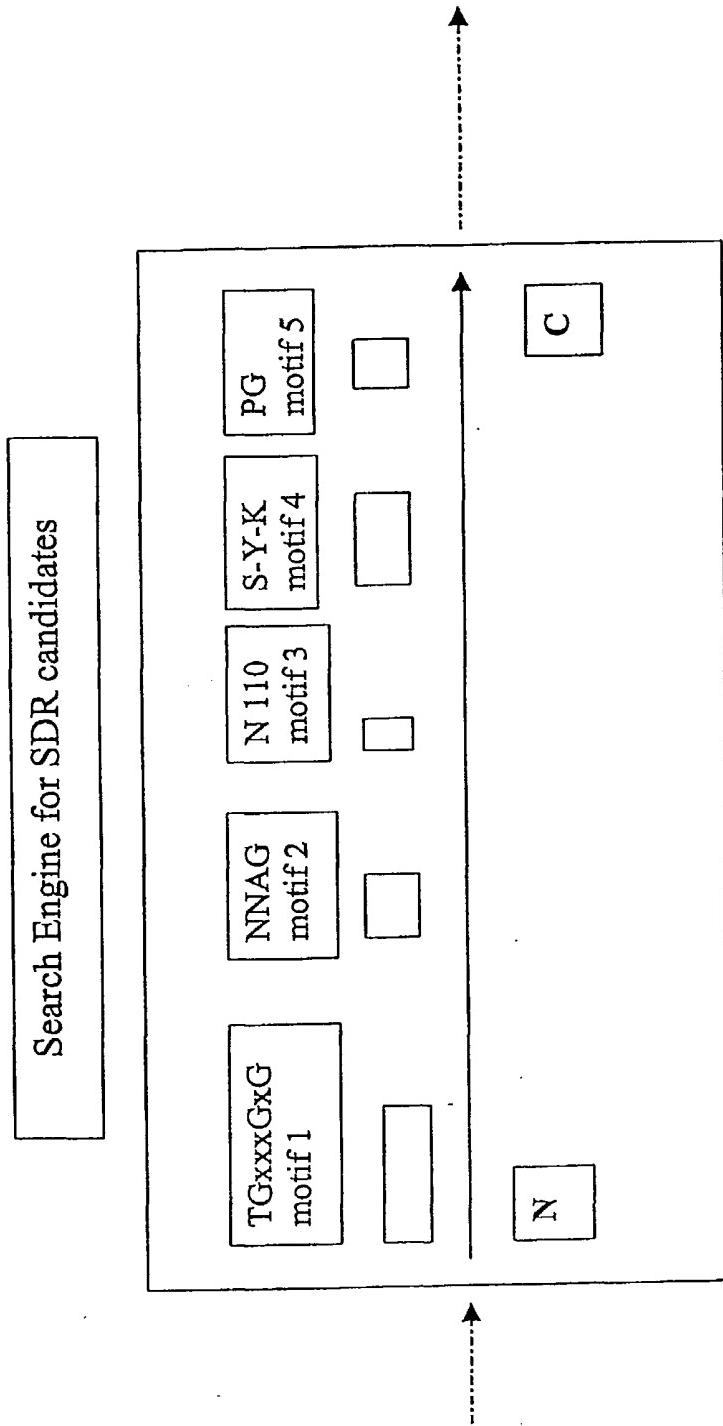
- 136 -

34. Pharmaceutical agent obtainable by a method according to any of claims 20-33.
- 5 35. Pharmaceutical agent according to claim 34 for the prophylaxis, treatment or/and diagnosis of diseases.
- 10 36. Pharmaceutical agent according to any of claims 34 or 35, which is a fungicide or antibiotic.
- 15 37. A method for detection of clinically relevant polymorphisms or single nucleotide polymorphisms comprising the steps
 - (a) providing one or more target sequences or members of the short chain dehydrogenase family based on an algorithm using core SDR motifs for searching members of the SDR family,
 - (b) ranking the members of the short chain dehydrogenase family according to the number of amino acids matching with the core SDR motifs applied, and
 - (c) comparing evolutionary patterns within the SDR enzymes.
- 20 38. The method according to claim 37, wherein disease mechanisms are characterised.
- 25 39. The method according to claim 37 or 38, wherein metabolisms of xenobiotics are characterised.
40. The method according to any of claims 37-39, wherein structure-function relationships are identified and/or substrates of SDR members with unknown function are identified.
- 30 41. The method according to claim 20-33, wherein a pharmaceutical agent for affecting immune regulation is provided by developing a modulator for 17 β HSD type 3, 17 β HSD type 7, 17 β HSD type 8, 17 β HSD type 10, 11 β HSD-1, CR1, UDP glucose epimerase, SDR_SRL, AF067174, AF151840, AF151844, AF0078850, Fvt-1, HEP-27, DKFZ_ORF, WWOX_ORF, or CR3.
- 35

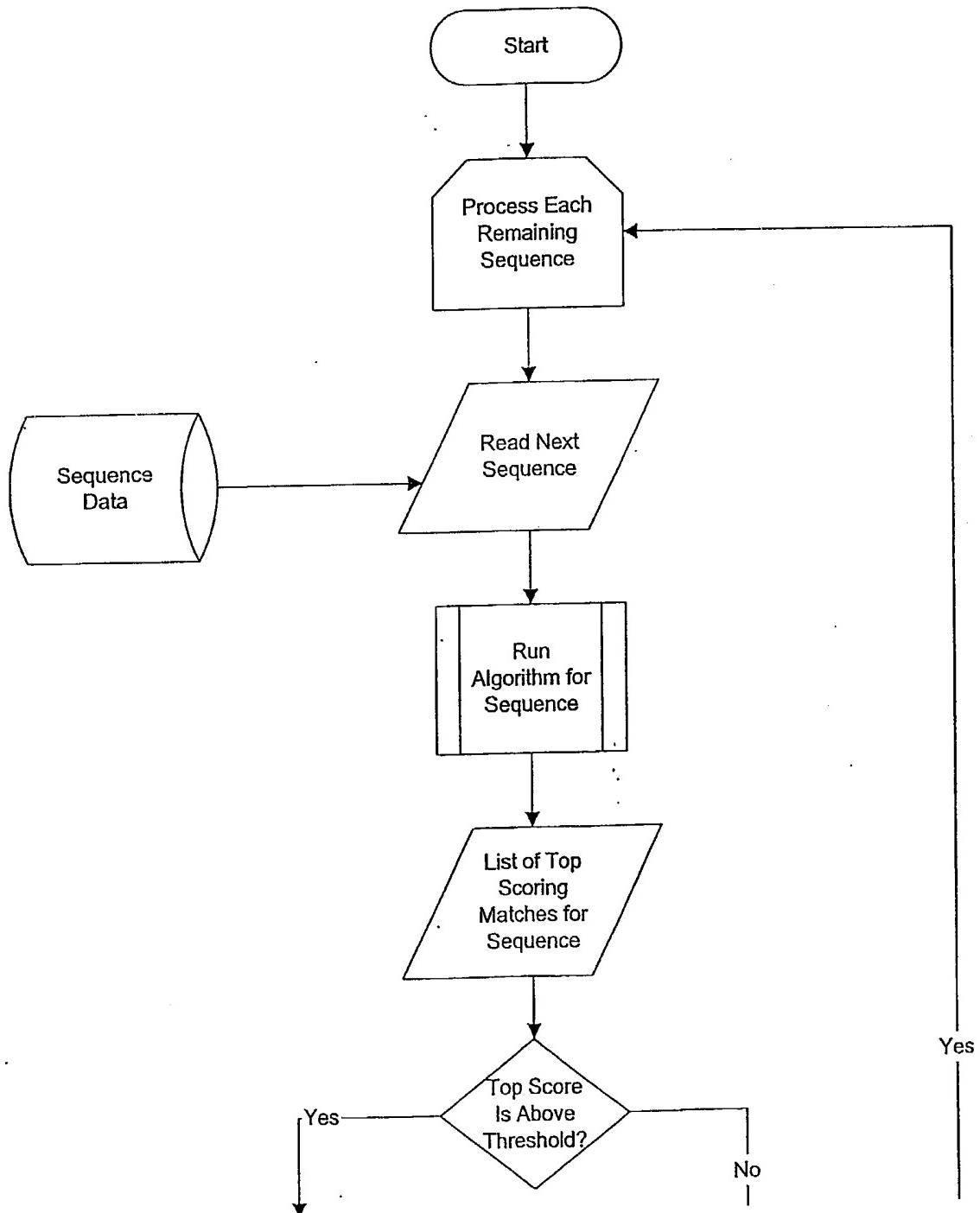
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42. The method according to claims 20-33, wherein a pharmaceutical agent for affecting autoimmunity is provided by developing a modulator for 17 β HSD-3, 17 β HSD-8, 11 β HSD-1, AF057034, U89717, CR1, AF0078850, HEP-27, or CR-3.
- 5
43. The method according to claim 20-33, wherein a pharmaceutical agent for wound healing or partial recovery is provided by developing a modulator for 17 β HSD-3, 17 β HSD-8, 11 β HSD-1, U89717, CR1, AF0078850, HEP-27, or CR-3.
- 10
44. The method according to claim 20-33, wherein a pharmaceutical agent for treatment of leukemia is provided by developing modulators for 17- β HSD-10 or Fvt-1.
- 15
45. The method according to claim 20-33, wherein a pharmaceutical agent for apoptosis regulation is provided by developing a modulator for 17 β HSD-10, U89717, SDR_SRL; or for providing a pharmaceutical agent for affecting immune response by providing a modulator for AF016509, or providing a pharmaceutical agent for the treatment of cancer by providing modulators for AF016509, or providing a pharmaceutical agent for affecting cell growth by providing a modulator for U89717, or providing a pharmaceutical agent for the treatment of lung carcinoma by providing a modulator for SDR_SRL, or providing a pharmaceutical agent for the regulation of inflammation or vasculitis by providing a modulator for DKFZ_ORF.
- 20
- 25

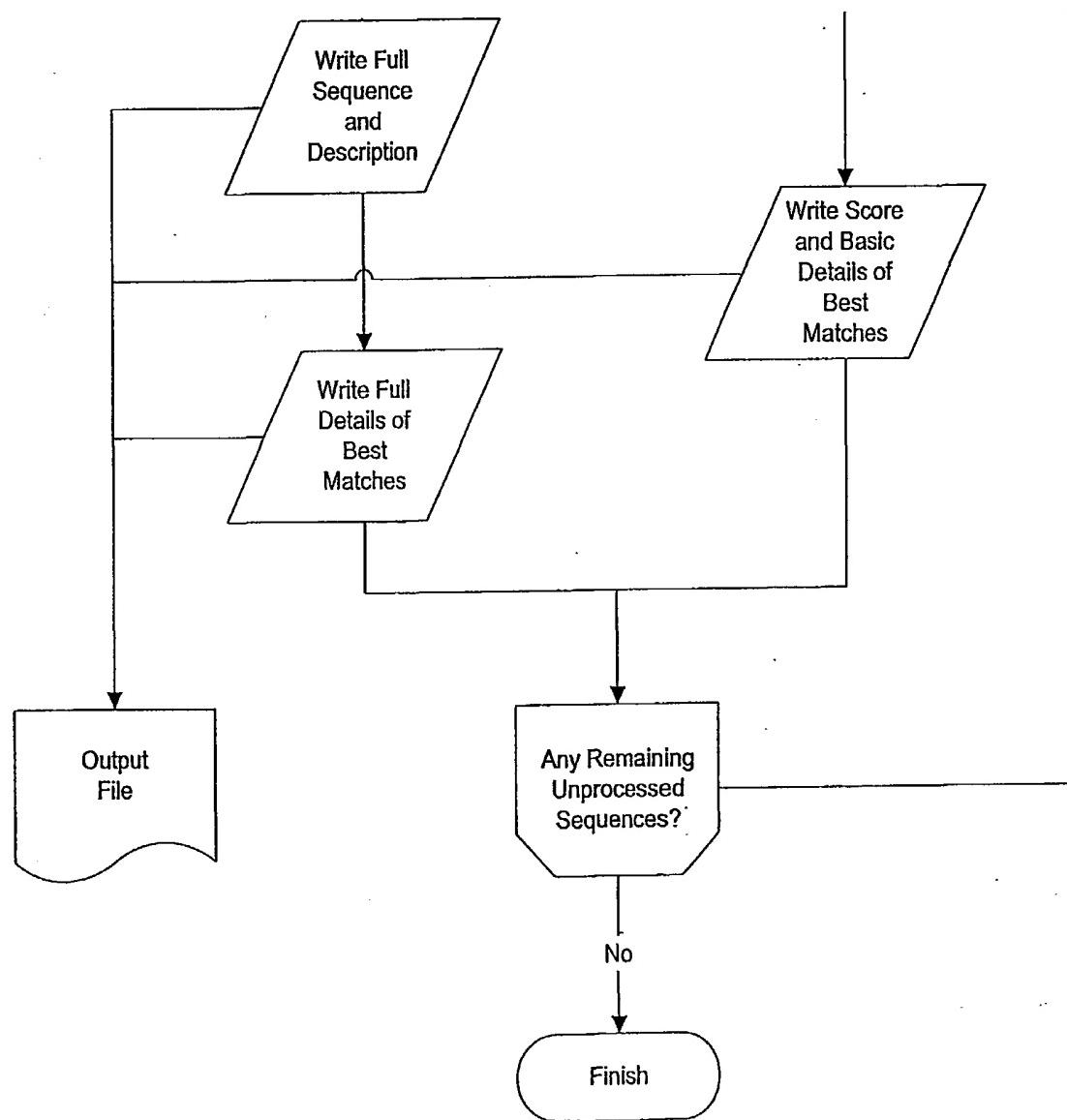
1/30

Fig. 1

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Flowchart for data processing**Fig. 2a**

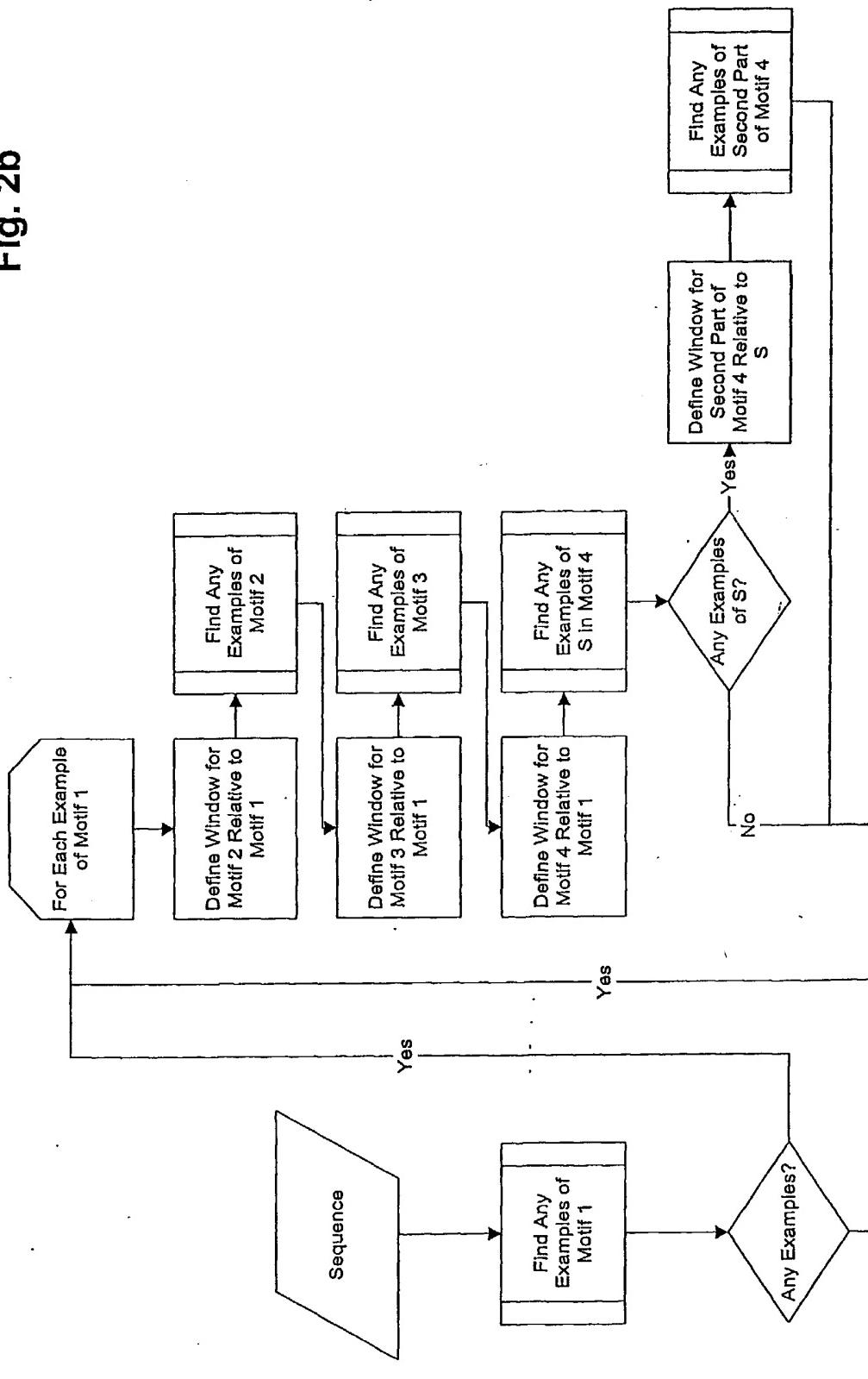
3/30

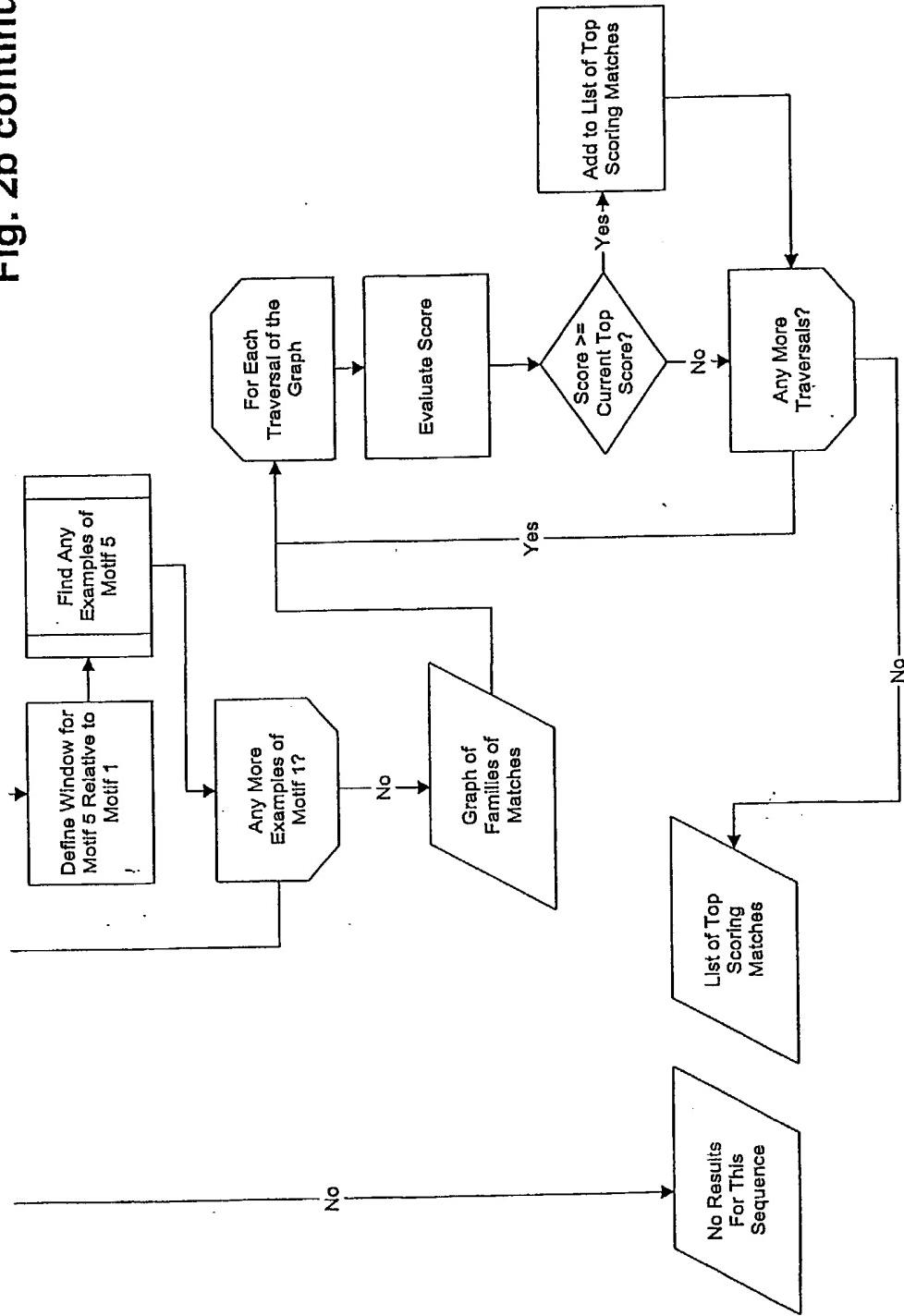
Fig. 2a continued

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Flowchart for the algorithm

Fig. 2b



Flowchart for the algorithm**Fig. 2b continued**

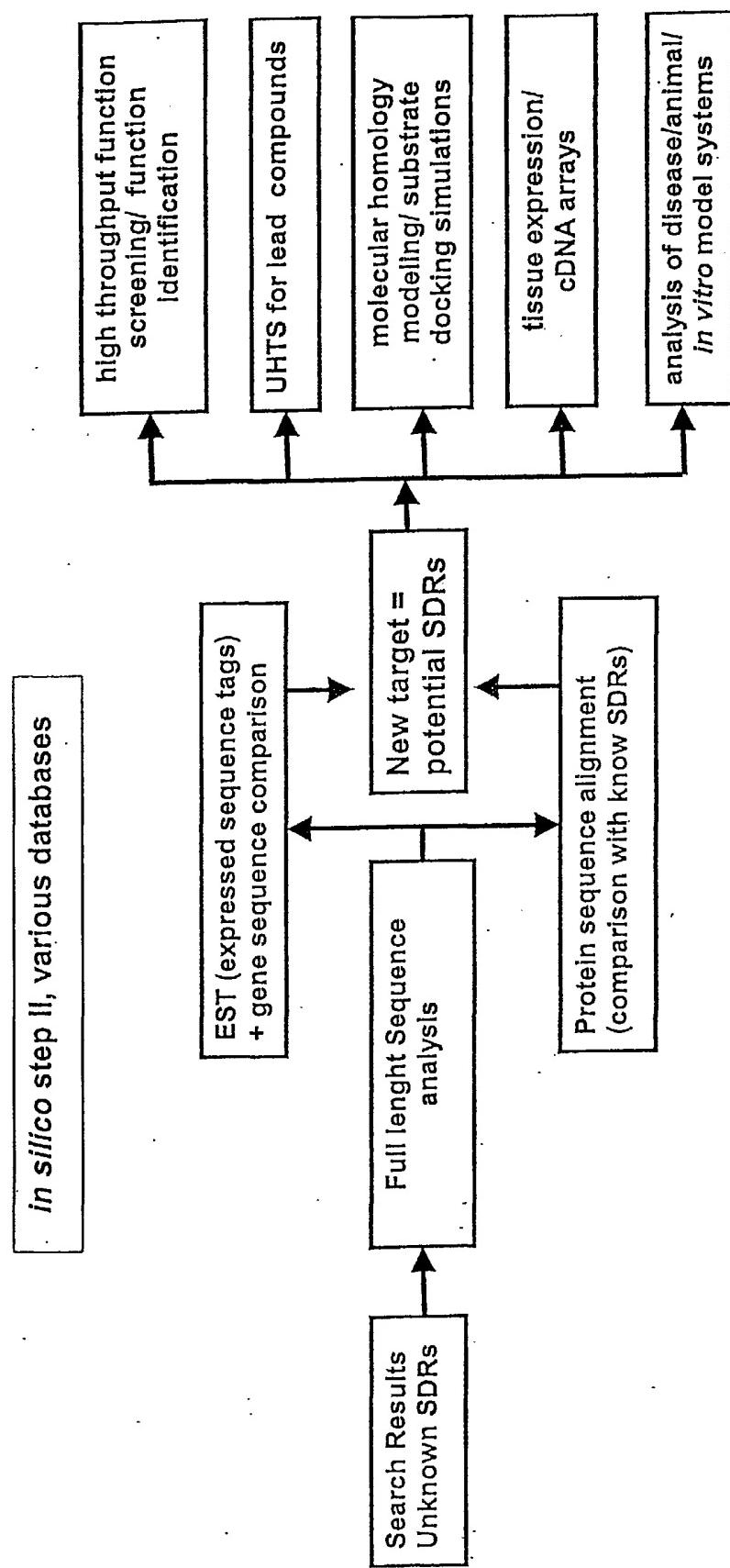


Fig. 3

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Fig. 4a-top left

M

CGI-93

DKFZ-ORF

CR-1

CR-3

SRL

Hep-27

SDH-RDH

RODH4

RDH

9cis-RDH

3beta-HSD-

3beta-HSD-

RDH_ORF

CGI-86

BDH

17beta-HSD

11beta-HSD

CR-AG

11cis-RDH

17beta-HSD

M S T F F S D T A W I C L A V P T V L
MER W P W P S G G A W L L V A A R A

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Fig. 4a-top middle

K L I D Y G L S G Y Q E S A E V K A M D F I T S T A I L P ²⁰ L F G C L G V F G L F - - - R ³⁰ L Q W V R - - G K A Y
 M V S P A T R K S L P K V K A M D F I T S T A I L P ¹⁰ L F G C L G V F G L F - - - R ⁴⁰ L Q W V R - - G K A Y
 .
 M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S M S S
 M L S A V A R G Y Q G W F H P C A R L S V R - - - M S S T G I D - - R K G V
 M W L Y L A V F V G L Y - - - Y L H W Y R - - E R Q V
 M W L Y L A V F V G L Y - - - Y L H W Y R - - E R Q V
 M W L Y L A A F V G L Y - - - Y L H W Y R - - E R Q V
 M W L P L L G A L L W - - - A V L W I L L R - - D R Q S

M L F W Y L G L L I L C - - - - - G F L W T R K - - - G K L K
 M N W E L L L W L L V L C A L L L V Q L L R F L R A D G - - - D L T L L W A E W Q G R R P
 G L R P P P G R F S R L P G K T L S A C D R E N G A R R p L L G S - - - T S F I P I G R R T Y A S A
 C G T V F C K Y K K S S G Q L W S W M V C L A G L C A V C L L I L S P F W G L L I L F S - - - V S C F L M Y T Y L S G Q E
 L L Q L L R S D L R L G R P L L A A L L A A L D W L C Q R L L P P A A L A V L A - - - A A G W I A L S R L A R P Q
 M M N F
 S Q L

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Fig. 4a-top right

LR - - - - - N A Y V V I L E S A T S I L K E C A K V F Y A A - - - A K L V E C G R N G G
 50 LR - - - - - N A V V V I L E S A T S I L K E C A K V F Y A A - - - A K L V E C G R N G G
 GI - - - - - H V A E V I L G N K I L A I V R D C R L F - - S G D V V E T A R D V T
 10 CS - - - - - R V A E V I L A N R S I L A I A R E C R Q F - - S G D V V L T A R D V A
 LA - - - - - N K Y A L V I A S T D I I F A I A R R A Q D - - A H V V V S S R K Q Q
 20 LA - - - - - N R Y A V V S T S I I I F A I A R R A R D - - A H V V I S S R K Q Q
 LS H - - - - - L R D K Y V F I C D S E F K L L A R Q D A R - - L R V L A A C L T E K
 30 L S H - - - - - L R D K Y V F I C D S E F K L L A R Q D A R - - L R V L A A C L T B K
 VSH - - - - - L Q D K Y V F I C D S E F K N L L A R Q D A R - - L R V L A A C L T E K
 LP - - - - - A S N A F V F I C D S E F R L L A L Q D Q K - - S F R V L A S C L T P S
 MT G W S C L V A G G F L I Q R I I R L E V K E K E L K E I R A L D K A F G P
 MG W S C L V A G G L L E Q R I I V R L E V E E K E L K E I R A L D K A F R P
 IED - - - - - I T D K Y I F I C D S E F N L A R T F D K K - - F H V I A A C L T E S
 EWE - - - - - L T D M V V W V A S S I E E L A Y Q S K L - - V S L V I S A R R V H
 50 AEP - - - - - V G S K A V L V C D S E F F S L A K H H S K - - F L V F A G C L M K D
 LLP - - - - - V D Q K A V L V G D C N L I H A L C K Y D E L - - F T V F A G V L N E N
 RLP - - - - - V A T R A V L E C D S E F K E T A K K D S M - - F T V L A T V L E L N
 ELF - - - - - L A G R R V L V A G K I R G T V Q A H A T - - A R V V A V S R T Q A
 EG - - - - - K I A L V A S R D I A E T A A R - - G K V I G T A T S E N
 QNR - - - - - L R S A L A E V A G S I I R A V S V R E A G E - - A T V A A C D L D R A

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Fig. 4a-bottom left

17beta-HSD	
17beta-HSD	
RALDH3	
trans-enoy	
DECR	
PGDH	
RALDI[2]	
11beta-HSD	
CGI-82	
WWOX	M A A L R Y A G L D D T D S E D E L P P G W E B R T K D G W V Y Y A N H T B E K T Q W E H P K T G K R K
Fvt-1	
17beta-HSD	
Incyte-ORF	
SD	
17beta-HSD	
SEPR	
17beta-HSD	
GALE	
DHPR	

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Fig. 4a-bottom middle

MGS
MAA

MAT
MAT

MASSWAKGRSYLA
MASSWAKGRSYLA

MKLPARVFF¹⁰TLGSRILPCGLAPRFFSYG²⁰T³⁰KILYQNT⁴⁰EAL - - - QSKF⁵⁰SP⁶⁰LQKAMLP

MKFLLDILLPLLIV¹⁰ - - - CSLESFVKLF²⁰IPKR
MAFMKYLLP¹⁰ILGL²⁰ - - - FMAYYY³⁰SANEFR
MVELMFPLL¹⁰PLLY²⁰MAA - - - PQIRKML³⁰SSGVCTS
RVAGDL⁶⁰PYGWEQETDEN⁷⁰GQVFVDH⁸⁰1NKRTTYLD⁹⁰PR¹⁰⁰L¹¹⁰AFTVDDNPTK¹²⁰PTTRQR¹³⁰YDG¹⁴⁰STTAM
MLLAAAFLVA¹⁰PV²⁰ - - - LLLYMW³⁰SP⁴⁰LISPK

M.A.A

M.E.G

M.A.A.A

MESALPAAGFL¹⁰YWVGAGTVAYLALR²⁰1SYSSLFTALRVWGVGN³⁰EAG
MGDVLEQFF¹⁰LTG²⁰LLVCLACLA³⁰KCVRFSRCV⁴⁰LLNYWKVL⁵⁰PKSF

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Fig. 4a-bottom right

P L R - - - F D G R Y V I E V I E A G A ¹⁰ L E R A Y A L A F A E R - - - A L V V V N D L G G D
 C R S - - - V K G L V A V I E G A S E L & L A T A E R E V G Q - - - A S A V E L D L P N S
 G T R - - - Y A G K Y V V V V I E G G R ²⁰ I A G I V R A F V N S - - - A R V V I C D K D E S
 P G L - - - L Q G Q V A I V I E G A T ³⁰ I K A I V K E E L E L - - - S N V V I A S R K L E
 P N S - - - F Q G K V A F I E G G T ⁴⁰ I L K G M T T L S S L - - - A Q C V I A S R K M D
 M H - - - V N G K Y A I V I E A Q ⁵⁰ I R A F A E A L L K - - - A K V A L V D W N L E
 R K S - - - V T G E I V E I E A G H ⁶⁰ I R L T A Y E F A K L - - - K S K L V L W D I N K H
 P E M - - - L Q G K V I V I E A S K I E R E M A Y H E A K M - - - A H V V V T A R S K E
 T V Q - - - L P G K Y V V V I E A N T I ⁷⁰ I K E T A K E E A Q R - - - A R V Y L A C R D V E
 E I L Q G R D F T G K Y V V V I E A N S I I I F E T A K S F A L H - - - A H V I I L A C R N M A
 P L A - - - L P G A H V V V I E G S S ⁸⁰ I K C I A I E C Y K Q - - - A F I T L V A R N E D
 M A R T V V I E I C S S I I I L H L A V R A A S D P S Q S F K V Y A T L R D L K
 P M N - - - G Q V C V V I E A S R I I R G I A L Q C K A - - - A T V Y I T G R H L D
 V G P - - - G L Q E W A V V I E S T D ⁹⁰ I K S Y A E E A K H - - - M K V V I I S R S K D
 L R S - - - M G Q W A V I E A G D ¹⁰⁰ I K A Y S F E E A K R - - - L N V V E I S R T L E
 G L G - - - R A V C E L I E A S R I F R T L A P L A S E L L S P S S V L V L S A R N D E
 M R K V V I E I S S I I L A L C K R L A E D D - E L H L C I A C R N M S
 M A E K V V I E V I E G A G Y I I S H T V L E I L E A - - - Y L P V V I D N F H N
 A A G - - - E A R R V C V V I E G R G A L S R C V Q A F R A R - - - N W W V A S V D V V E N

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Fig. 4b-top left

CGI-93 - - - - - A **P**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ R E I R E I R E I T A S H A T K V Q T H K P Y L V T F **D**₁₂₀ L T D S G A I V - - - A A A A E I -
 DKFZ-ORF - - - - - A **I**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ **E**₉₀ R E I R E I R E I T A S H A T K V Q T H K P Y L V T F **D**₁₂₀ L T D S G A I V - - - A A A A E I -
 CR-1 - - - - - R G Q A A V Q Q **Q**₆₀ A - - - - - E G L S P R F H Q L D I D **D**₆₀ L Q S I R - - - A L R D F L -
 CR-3 - - - - - R G Q A A V Q Q **Q**₆₀ A - - - - - E G L S P R F H Q L D I D **D**₆₀ L Q S I R - - - A L R D F L -
 SRL - - - - - N V D Q A V A T **Q**₆₀ Q G - - - - - E G L S M V T G T M C H V G K A E D R E - - - R L V A M A -
 Hep-27 - - - - - N V D R A M A K **Q**₇₀ L Q G - - - - - E G L S M V A G I V C H V G K A E D R E B - - - Q L V A K A -
 SDH-RDH - - - - - G A E Q **Q**₇₀ R G Q T S D - - - - - R L B T **M**₈₀ T L D M T K T B S V A A A - - - Q W V K E C -
 RODH4 - - - - - G A E Q **Q**₇₀ R G Q T S D - - - - - R L E T **M**₈₀ T L D M T K T B S V A A A - - - Q W V K E C -
 RDH - - - - - G A E Q **Q**₇₀ R G Q T S D - - - - - R L E T **M**₈₀ T L D M T K M E S I A A A T - - - Q W V K E H -
 9cls-RDH - - - - - G A E D **Q**₇₀ Q G V A S S - - - - - G F N T T L L D I T **D**₉₀ P Q S F Q Q A A - - - K W V E M H -
 3beta-HSD- - - - - E L R E E F S K **Q**₅₀ N K T K L T V L E G D I I D E P F L K R A C Q D V S V I I H T A C I I D
 3beta-HSD- - - - - E L R B E F S K **Q**₅₀ N R T K L T V L E G D I I D E P F L K R A C Q D V S V V I H T A C I I D
 RDH_ORF - - - - - G S T A **K**₇₀ A E T S E - - - - - R L R T **V**₁₀₀ L L D M T D P E N V K R T A - - - Q W V K N Q -
 CGI-86 - - - - - E L R V K R C L E N - - G N L K E K D I I L V L P L D **T**₁₁₀ G S H E - - - A A T K **A** V -
 BDH - - - - - K G H D - - G V K **E**₁₂₀ D S I N S D - - - - - R L R T **M**₁₃₀ Q L N M F R S B E V E K V V G D - C P F E P E -
 17beta-HSD G P - - - G A E B **E**₁₂₀ R R T C S P - - - - - R L S V L Q M D I T K P V Q I K D A Y - - - S K V A M -
 11beta-HSD S P - - - G A I B **E**₁₃₀ R T C C S P - - - - - R L R L L Q M D L T K P G **D**₁₄₀ I S R L L - - - E F T K A H -
 CR-AG - - - - - D I D S E V R E C P G - - - - - I E P V C V D W B A T E R A L - - - - -
 11cls-RDH - - - - - G A Q A I S D Y **G**₅₀ A N - - - - - G K G L M L N **M**₆₀ T D P A S I E S V L - - - - - E K I -
 17beta-HSD - - - - - A A Q E T V R L **G**₅₀ G G P - - G S K E G P P R G N H A A F Q A D V S E A R A R C L L E Q V -

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Fig. 4b-top middle

L Q C F G Y V D I L V S - - - - -
 140
 140 L Q C F G Y V D I L V S - - - - -
 140 R K E Y G G I D V L V S - - - - -
 90 R K E Y G G I N V L V S - - - - -
 90 V K L H G G I D I L V S - - - - -
 140 L E H C G G V D F I L V C S - - - - -
 140 V R D K G - L W G I L V S - - - - -
 140 V R D K G - L W G I L V S - - - - -
 140 V G D R G - L W G I L V S - - - - -
 140 V K E A G - L F G I L V S - - - - -
 90 V F G V T H R E S I M V N V - - - - -
 100 V F G V T H R E S I M V N V - - - - -
 110 V G E K G - L W G I L V S - - - - -
 140 L Q E F G R I D I L V S - - - - -
 140 G P E K G - M W G I L V S - - - - -
 140 L Q D R G - L W M A V I L V S - - - - -
 140 T T S T G - L W G I L V S - - - - -
 80 - G S V E P V D I L V S - - - - -
 80 R A E F G E V D I L V S - - - - -
 90 Q A C F S R P P S V V V S - - C - - - - -
 140 I S Y R - - - - -
 140 I S Y R - - - - -
 140 I A F K V - - - - -
 90 A V A P K S - - - - -
 100 A V N P F F - - - - -
 140 V N p L V - - - - -
 140 I S L P T - - - - -
 140 I S L P T - - - - -
 140 I L T P I - - - - -
 140 V A G I I - - - - -
 140 K E T Q L L - - - - -
 100 K E T Q L L - - - - -
 110 E A C V Q A S V P V F I - - - - -
 120 E A C V Q A S V P V F I - - - - -
 120 A P T D W L - T L E D Y - - - - -
 140 S L C M D T - S L D V Y - - - - -
 140 G E V E F T - S L E T Y - - - - -
 140 T D G E L L - L M T D Y - - - - -
 140 A D A E L S - P V A T F - - - - -
 90 Q P F L E V - T K E A F - - - - -
 100 N L L M R M - K D E E W - - - - -
 110 E F L L H M - S R D D W - - - - -
 140 G S L M D V - T E E V W - - - - -
 140 G S T L G T - S E Q I W - - - - -
 120 A P N E L L - T K Q D F - - - - -
 130 A P N E L L - T K Q D F - - - - -
 120 T L C E W L - N T E D S - - - - -
 120 G P T P W L - T R D D F - - - - -
 120 E A C V Q A S V P V F I - - - - -
 120

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Fig. 4b-top right

- K R V M E T ¹⁰⁰ - - Y F - G P V A L T K A L L P S M I K R R - - Q ¹⁰⁰ - - - - - H I V A I S
 | K R V M E T ¹¹⁰ - - Y F - G P V A L T K A L L P S M I K R R - - Q ¹¹⁰ - - - - - H I V A I S
 | E V T M K T ¹²⁰ - - F F - G T R D V C T E L L P L J K P - - Q ¹²⁰ - - - - - R V V N V S
 - E M T L K T ¹³⁰ - - F F - A T R N M C N E L L P I M K P - - H ¹³⁰ - - - - - R V V N I S
 - D K T L D I ¹⁴⁰ - - V K - A P A L M T K A V V P E M E K R - - G ¹⁴⁰ G - - - - - S V V I V S
 - D K I I L S V ¹⁵⁰ - - V K - S P A L L S Q L L P Y M E N R - - R ¹⁵⁰ - - - - - A V I L V S
 - V T I I L D V ¹⁶⁰ - - L L - G V I D V T L S L L P L V R K A - - R ¹⁶⁰ - - - - - R V V N V S
 - V T I I L D V ¹⁷⁰ - - L L - G V I D V T L S L L P L V R K A - - R ¹⁷⁰ - - - - - R V V N V S
 - M N M L K Y ¹⁸⁰ - - L L - G V I Q V T L S M L P L V R R A - - R ¹⁸⁰ - - - - - R I V N V S
 - Q R V L N V ¹⁹⁰ - - T M - G P I G V T L A L L P L L Q Q A - - R ¹⁹⁰ - - - - - R V I N I T
 - Y T S S I E - V A G P N S
 - Y T S S I E - V A G P N S
 - R E P I E V ²⁰⁰ - - L F - G L I S V T I L N M L P R P Q E D Q P G Q ²⁰⁰ G - - - - - T T L P S P
 - R K L I E L ²¹⁰ - - Y L - G T V S L H K C V L P H M I E R K - - Q ²¹⁰ - - - - - K I V T V N
 - K Q V A E V ²²⁰ - - L W - G T V R M T K S F L P L I R R A - - K ²²⁰ - - - - - R V V N I S
 - K Q C M A V ²³⁰ - - F F G T V E V H K T F L P L L R K S - - K ²³⁰ - - - - - R L V N V S
 - R S C M E V ²⁴⁰ - - F F G A L E T K G L L P L L R S S - - R ²⁴⁰ - - - - - R I V T V G
 - D R S F E V ²⁵⁰ - - T R A V I Q V S Q I V A R G L I A R G - V P ²⁵⁰ - - - - - A I V N V S
 - N D I I E T ²⁶⁰ - - L S S V F R L S K A V M R A M M K K R - - H ²⁶⁰ - - - - - R J I T I G
 - D K V I A V ²⁷⁰ - - L K G T F L V T Q A A Q A L V S N G - C R ²⁷⁰ - - - - - S I I N I S

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Fig. 4b-bottom left

17beta-HSD F K G V G K G S L A A D K V V E E - - - - - I R R R G G K A M A N Y D S V E E G E - - - - - K V V K T A -
 17beta-HSD - - - - - G G I A Q A K K G N - - - - - N C V R A P A D V T S E K D V Q T A L - - - - - A L A -
 RALDH3 - - - - - G G R A I E Q E P G - - - - - A V F I L C D W T Q E D D V K T L V - - - - S - - E T -
 trans-enoy R L K S - - A A D E I Q A N E p p - - - - T K Q A R X I P I Q C N I R N E E B V N - - - - N L V K S T -
 DECR - - - - - V I K A T A B Q I S S - - - - Q T G N K X H A I Q C D E V R D P D M V Q - - - - N T V S E L -
 PGDH - - - - - A G V Q C K A A I H E Q - - - - F E P Q K T L F I Q C D E V A D Q Q Q L R - - - D T F R K V -
 RALDH2 - - - - - G P E E T A A K C K G - - - - L G A K X H T F X Y D C S N R E D I Y - - - S S A R K V -
 Libera-HSD - - - - - T L Q K V V S H C L E L - - - - G A A S A H Y I A G T M E D M T P A E - - - Q F V A Q A -
 CGI-82 - - - - - K G E L V A K E I Q T T - - - - T G N Q Q Q M L V R K L D L S D T K S I R - - - A F A K G F -
 WWOX R - - - - - A S I A V S R I I E E W - - - - H K A K X H A M T L D L A L L R S V Q - - - H F A E A F -
 Fvt-1 - - - - - K E L Q A K K E I E M H S I N - - D K Q V V V L C I S Y D V S Q D Y N Q V E - - - N V I T K Q A -
 17beta-HSD T Q G - - R E W E A A R A A C P - - - - P G S L E T L Q L D V R D S K S V A - - - A A R E -
 Incyclo-ORF - - - - - T L R V V A Q E A Q S - - - - L G G Q Q C V P V Y C D S S Q E S E V R - - - T L F E Q V D
 SD - - - - - K E D Q V S S H I K E K - - - - F K V E T R T I A V D F A S E D I Y D - - - K I K T G -
 17beta-HSD - - - - - K E E H A I A T E I E R T - - - - T G R S M K I I Q A D F T K D D I Y E - - - H I K E K -
 SEPR - - - - - A E R Q I B A B I G A B - - - - R S G L R M V R V P A D L G A E A G L Q Q L L G A L R E L P
 17beta-HSD - - - - - K A E H A V C A A L A S - - - - H P T A B M T I V Q V D V S N L Q S V F - - - R A S K E L -
 GALE - - - - - A F R G G G S L P E S L - - - - R R V Q B E L T G R S V B F E E M D I L D Q G - - - A L Q R L F
 DHPR - - - - - E E A S A T I I V K - - - - M T D S R T E Q A D Q V T A E V G K - - - L L G E - -

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Fig. 4b-bottom middle

L D A F **G R I D V V V**₉₀ - - - - - I L R D - - - - - R S F A R I - S D E D W - - - - -
 K G K F **G R V D V A V P C**₉₀ - - - - - I A V A S K T Y N L - - - - - K K G Q T H - T L E D F - - - - -
 I R R F **G R L D C V V**₉₀ - - - - - H H P P P - - - - - Q R P E E T - S A Q G F - - - - -
 L D T F **G K I N F L V**₁₀₀ - - - - - G G Q F L - - - - - S P A E H I - S S K G W - - - - -
 I K V A **G H P N I V I**₁₀₀ - - - - - A G N F I - - - - - S P T E R L - S P N A W - - - - -
 V D H F **G R L D I L V**₉₀ - - - - - V N N E - - - - - - - - - - - K N W E K - - - - -
 K A E I **G D V S I L V**₁₀₀ - - - - - V V Y T - - - - - S D L F A - T Q D P Q I - - - - -
 G K L M **G G L D M L I L**₁₀₀ - - - - - H I T N T S L - - - - - N L F H D D - I H H V R - - - - -
 L A E E K H L H V L I ₁₀₀ - - - - - V M M C - - - - - P Y S K - T A D G F - - - - -
 K A K N V P L H V L V C ₁₀₀ - - - - - A T F A L - - - - - P W S L - T K D G L - - - - -
 Q E K I **G P V D M I L V C**₁₀₀ - - - - - A M A V S - - - - - G K F E D L - E V S T F - - - - -
 R V T E **G R V D V L V C**₉₀ - - - - - L G L L - - - - - G P L E A L - G E D A V - - - - -
 R E Q Q **G R E D V L V**₉₀ - - A Y V Q T I L - - - - - N T R N K A - F W E T P A - - - - -
 - L A G L E I G I L V ₁₀₀ - - V E M S Y E Y - - - - - P E Y F L D V P D L D N V I - - - - -
 - L A G L E I G I L V ₁₀₀ - - V E M L P N - - - - - L L P S H F L N A P D E I - - - - -
 R P K G L Q R L L I ₁₀₀ - - S L G D V - - - - - S K G F V D L - S D S T Q V - - - - -
 K Q F Q R L D C I Y L ₉₀ - - I M P N P Q L N I K A L F P F G L F S R K V I H M F S T A E G L L T Q G D K I T A D G
 K K Y S F - - M A V I H F - - L K A V G - - - - - E S V Q K P L D Y Y R V N L T G T I Q L E I
 - E K V D A I L C V A G G - - W G N A K S - - - - - K S L F K N - C D L M W - - - - -

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Fig. 4b-bottom right

- D I I H R V H - - L R G S S F Q V T R A W E H M K K Q K - - Y ¹³⁰ - - - - - R I I M T S
 - Q R V L D V ¹²⁰ - - L M G T F N V I R L V A G E M Q Q N E P D Q G G Q R - - - G V I I N T A
 - R Q L L E L ¹¹⁰ - - L L G T Y T L T K L A L P Y L R K S - - Q ¹²⁰ - - - - - N V I N N I S
 - H A V L E T ¹³⁰ - - L T G T F Y M C K A V Y S S W M K E - - H ¹³⁰ G - - - S I V N J I
 - K T I T D I V - - L N G T A F V T I L E I G K Q L I K A Q - - K ¹³⁰ - - - - - A A F L S I T
 - - T L Q I E - - L V S V I S G T Y L G L D Y M S K Q N G G E ¹²⁰ G - - - - - I I I N M S
 - E K T F E V ¹⁴⁰ - - V L A H F W T T K A F L P A M T K N N - - H ¹³⁰ - - - - - H I V T V A
 - - K S M E V ¹⁴⁰ - - F L S Y V V L T V A A L P M L K Q S - - N C ¹²⁰ - - - - - S I V V V S
 - E M H I G V ¹³⁰ - - H L G H F F L L T H L L E K L K E S - - A P S - - - - - R I V N V S
 - B T T F Q Y ²¹⁰ - - H L G H F Y L V Q L L Q D V L C R S A P A R V I V V S S E S - H R F T D I N
 - E R L M S I ¹⁴⁰ - - Y L G S V Y P S R A V I T T M K E R R - - V ¹⁶⁰ - - - - - R I V F V S
 - A S V L D V E ¹¹⁰ - - V V G T V R M L Q A F L P D M K R R G - - S ²⁰⁰ - - - - - R V L V T G
 - S M W D D I ¹⁷⁰ N V G I L R G H Y F C S V Y G A R L M V P A G - - Q ¹³⁰ - - - - - L I V V I S
 - K K M I N I ¹⁶⁰ - - I I L S V C K M T Q L V L P G M V E R S - - K ¹²⁰ - - - - - A I I L N I S
 - Q S L I H C D ¹⁶⁰ - - I T S V V K M T Q L I I K H M E S R Q - - K ¹³⁰ - - - - - L I I L N I S
 - N N Y W A L E ¹³⁰ - - L T S M L C L T S S V L K A F P D S - - P ¹⁴⁰ - - - - - L N R T V V N T S
 - L Q E V F E T N ¹⁴⁰ - - V F G H F I L I R E L E P L L C H S D - N P S - - - - - Q L I W T S
 M K A H G V K ¹²⁰ - - L V F S - - - - - - - - - - - S S
 - K Q S I W T S ¹¹⁰ - - T I S S H L A T K H L K E G - - - - - L L T L A G

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Fig. 4c-top left

CGI-93	I Q G K M - - S I P F R - - - - -
DKFZ-CRF	I Q G K M - - S I P F R - - - - -
CR-1	I M S V R - - A L K S C - - - - -
CR-3	L Q C L R - - A P E N C - - - - -
SRL	I A A F S - - P S P G F - - - - -
Illep-27	I A A Y N - - P V V A L - - - - -
SDH-RDH	V M G R V - - S L F - G - - - - -
RODH4	V M G R V - - S L F - G - - - - -
RDH	I L G R V - - A F F - V - - - - -
9cis-RDH	V L G R L - - A A N - G - - - - -
3beta-HSD-	Y K E I I Q N G - H E E P L E N T W - - - - -
3beta-HSD-	Y K E I I Q N G - H E E P L E N T W - - - - -
RDH_ORF	C T A G K L P - S V G - - - - -
CGI-86	I L G I I - - S V P L S - - - - -
BDH	M L G R M - - A N P A R - - - - -
17beta-HSD	M G G G A - - P M E R L - - - - -
11beta-HSD	P A G D M - - P Y P C L - - - - -
CR-AG	Q C S Q R - - A V T N H - - - - -
11cis-RDH	V V G T M - - G N G G Q - - - - -
17beta-HSD	I V G K V G - N V G - Q - - - - -

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Fig. 4c-top

T K K G V H Q K E G W P S S A M G V T I G - - - - - S A M A X S E H M - - - - - T Q A F F D C L R A E M E Q - - - - - Y E I E V T V I S Y I - - - H
 T K N E V H E R E G W P N S P R G V S A L G - - - - - V T V L S R I L A R R L D E - K R K A D R I L V N A C C S E P V K T D middle
 T N W A S S A G - - - - - S P N V S S T A Y - - - - - L L G L T K T D A I E L A P - - - - R N H R V N C L A M L I - - - K
 G V E N V S S T A Y - - - - - L L G L T R T D A L E L A P - - - - K D I E R V N C V V V S I I - - - K
 G G C C I S R Y G - - - - - V E A F S D S I R R E L S Y - - - - F G Y K V A M I E F Y F - - - K
 G G Y C I S R Y G - - - - - V E A F S D S I R R E L S Y - - - - F G Y K V A M I E F Y F - - - K
 G G M C V S R Y G - - - - - V E A F S D I L R R E I Q H - - - - F G Y K I S I V E Y F - - - R
 G G M C V S R Y G - - - - - V E A F S D I L R R E I Q H - - - - F G Y K I S I V E Y F - - - R
 P A P P P H I S K K L A E K A V L A A N G W N L K N G G T L Y T C A L R P M Y I Y G E G S R F L S A
 P T P P P Y S S K K L A E K A V L A A N G W N L K N G D T L Y T C A L R P T Y I Y G E G E P F L S A
 G G E T P S S Y M - - - - - V E G F N D S L R R D M K A - - - - F G Y H V S C L E F M L F - - - K
 I G A C A S S H M - - - - - L R G F F N G L R T E L A T - - - Y P G L I V S N A C F E P V - - - Q
 S P N C I T F G - - - - - V E A F S D C L R Y E M Y P - - - - L G Y K Y S V V E F S N F I A A
 A S M G S S S A A - - - - - V T M P S S V M R L E S K - - - - W G T K V A S I Q F G F L T N
 G A W G T S S A M - - - - - V A L L M D T W S C E R L P - - - - W G Y K Y S I L Q F G C F K - T
 S V S C S T R G A A - - - - - L D M L T K V M A L E F G P - - - - H K J R V N A V N E T V V - - - M
 A N G A A A A R A G - - - - - L I G F S K S L A R E V A S - - - R G I T V N V V A F I - - - E
 T N W A S S A G - - - - - V I G L T Q T A A R E L G R - - - - H G I A P C N I S V L F 1 - - - A

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Fig. 4c-top right

T N L S - - - - - V N A I T A D G S R - - - - - Y G V M D T T T A Q A E A L - W R W P R M E
 T N L S - - - - - V N A I T A D G S R - - - - - C G V M D T T T A Q G R S P - V E V A Q D V
 M A G P K A T K S P - E E G A E T P V - - Y L A L L P P D A E G P H G Q F V S E K R V E Q W - -
 M D G K D S I R T V - E E G A E T P V - - Y L A L L P P D A T E P Q G Q L V H D K V V Q N W - -
 T S F S - - - - - R M L W M D K E K E - - - E S M K B T L R I R R L G E P B D C A G I V
 T D F S - - - - - K V F H G N E S L W - - - K N F K B H H Q L Q R I G E S B D C A G I V
 T A V T S K E - - - R F L K S F F L E I W D R S S P E V K E A Y G E K F V A D Y K K S A E Q M
 T A V T S K E - - - R F L K S F F L E I W D R S S P E V K E A Y G E K F V A D Y K K S A E Q M
 T G M T N M T - - - Q S L E R M K Q S W K E A P K H I K E T Y G Q Q Y F D A L Y N I M K E G
 T P V T N L E - - - S L E K T L Q A C W A R L P P A T Q A H Y G G A F L T K Y L K M Q Q R I
 S I N E A L - - - N N N G J I L S S V G - K F S T V N P V Y V G N V A W A H I L A L R A L Q D
 S I N E A L - - - N N N G J I L S S V G - K F S T V N P V Y V G N V A W A H I L A L R A L R D
 T N L A D P V - - - K V I E K K L A I W E Q L S P D I K Q Q Y I B K S L D K L K G N
 S N I V - - - E N S L A G E V T K - - - T I G N N G D Q S H K M T T S R C V R L M
 T S L Y N P E - - - S I Q A I A K K M W E E L P E V V R K D Y G K K Y F D E K I A K M E T Y
 T A G T S - D - - - K W E K L E K D J L D H L P A E V Q E D Y G Q D Y I L A Q R N F L L I
 E S V R N V G - - - Q W E K R K Q L L A N L P Q B L L Q A Y G K D Y I B H L H G Q F L H S
 T S M G - - - Q A T W S D P H K A - - - K T M L N R I P L G K F A E V E H V V N A I
 T D M T - - - R A L S D D Q R A G - - - K T M L N R I P L G K F A E V E H V V N A I
 T P M T - - - K K V P K K V V D K - - - I T E M I P M G H L G D P E D V A D V V

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Fig. 4c-bottom left

I7beta-HSD	A S G I Y G - N F G - Q -
I7beta-HSD	V A A F E G - Q V G - Q -
RALDH3	L V G A I G - Q A Q - A -
trans-enoyl	V P T K A G - - - F P L A V H S G A R A -
DECR	T I Y A E T - - G S G F V V P S A S A K A -
PGDH	L A G L M - - P V A Q Q -
RALDH2	A A G H V - - S V P F L -
I1beta-HSD	I L A G K V - - A Y P M V -
CGI-82	L A H H L G - R I H F H N L Q G E K F Y N A G -
WWOX	D S L G K L D - F S R L S P T K N - - D Y W A M -
Fv1-I	Q A G Q I G - L P G F T -
I7beta-HSD	V G G L M - - G L P F N -
Incyclo-ORF	P G S L Q Y - M F N -
SD	G S G M L - - P V P L L -
I7beta-HSD	G I A L F - - P W P L Y -
SEPR	L C A L Q - - P F K G W -
I7beta-HSD	R S A R K S - N F S L E D F Q H S - - K G K -
GALE	A T V Y G N P Q Y L P D E A H P T G G C T N -
D1IPR	A K A A L D - - G T D G M -

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Fig. 4c-bottom middle

170 - - - - - A N E S I K A E L G - - - - - L L G L A N S L A I E G R K - - - S N H C N T I A F N A G - - S q
 175 - - - - - A A M S A S S G G - - - - - I V G M T L P I A R D Q A P - - - I G I R Y M T I A R G L F G - - T
 180 - - - - - V P R V E T T G A - - - - - V T A M T K A E L D E S P - - - Y G Y R V N C I S E A N I - - W
 185 - - - - - G V S N L T R S L - - - - - A L E W A C S - - - - - G I R I N C V A D A V I Y S Q
 190 - - - - - G V R A M S E S L - - - - - A A E W G K Y - - - - - G M R F I N V I Q P I K T K
 195 - - - - - P V N C A S S H G - - - - - I V G F T R S A A L A A N L M N - S G V R L N A I C H F V N T A
 200 - - - - - L A M C S S F A - - - - - A V G F H K T L T D E Q A A L Q I T G V K T T C L C N F V - - N
 205 - - - - - A A M S A S S F A - - - - - L D G F F S S I R K E Y S V S R - V N V S I T L C V L L I D T E
 210 - - - - - L A M C H S S L A - - - - - N I L E T Q E L A R R I K G - - - S G Y T T Y S V H T V - - Q
 215 - - - - - L A M N R S P L C - - - - - N I L F S N E I H R R I S P - - - R G V T S N A V H R N M M Y S
 220 - - - - - A N S A S S F A - - - - - I R G L A E A L Q M E V K P - - - Y N Y Y I T V A Y R P D T D T P
 225 - - - - - D V M C A S S F A - - - - - L E G L C B S I A V L I L P - - - F G Y H L S L I E C S P V H T A
 230 - - - - - V P R G V C A A - - - - - C D K L A A D C A H E L R R - - - H G Y S C V S L W S I V Q T E
 235 - - - - - T I M S A T T R - - - - - Y D F E S Q C L H E Y R S - - - K G V F Y Q S V L E Y F V A T K
 240 - - - - - S M E S A S S A F - - - - - V C A E S K A L Q E E Y K A - - - K E Y I I Q V L T Y A V - - S
 245 - - - - - A L E C A G G A A - - - - - R D M L F Q V I L A E E P N - - - V R V L N Y A - - P L - - D
 250 - - - - - E P S S S R Y E A - - - - - T D L L S V A I N R N F N Q - - - Q G L Y S N V A C E S T A L T N
 255 - - - - - P R G K S I F R - - - - - I E E M I R D H C Q A D K T W N V V L L - R Y F N P T A H A S G
 260 - - - - - I G S G M A E G M - - - - - Y H Q L C Q S I I A G K N S G - - - - - M P E A A A I A

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Fig. 4c-bottom right

RMTQ - - - - - TV - MPEDLVE - - - - - ALKPEYYVAPLVLWLCHESCEE
 PLLT - - - - - SLP EKVVCNFL - - - - - ASQVPFPSRLGDPAEYAHLV
 PPLWEEL - - - - - AALMPDPRAS - - - - - REGMLAQPLGRMGQPAEVG
 AVEN - - - - - YGSWGGQSFFEG - - - - - SFQKIPAKRIGVPEEVSSVV
 GAFS - - - - - RLDPGTFEK - - - - - EMIGRIPCGRLGTVEBLANLA
 LBSIEK - - - - - ENMGQYIEYK - - - DHIKDMIKYYGILDPPLIANGL
 GFKNP - - - - - STSLGPTLEP - - - EEVVNRLMHGILTBQKMFIPS
 AMKAVS - - - - - GI VHMQAAPK - - - BECALEIIKGGAQBEVYYDS
 SELVRHS - - - - - SFMRWMWWLFS - - - FFIKTPQQGAQTSLHCALTBGL
 NHRSWW - - - - - VYTLLFTLAR - - - PFTKSMQQGAATTVYCAAPEL
 GAENR - - - - - TKPLETRLISETTSVCKPEQVAKQIVKDAAIQGNFNS
 FMEKVLGSPPEVLDRTDIHTFHRFYQYLAHSKQVFRBAAQNPPEEVF
 LLKEHMAK - EEVVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNILS
 LAKIR - - - - - KPTLDKPSPE - - - TFKSAIKTVGLQSRNTNGYL
 LAMT - - - - - KYLNNTNVITKT - - - ADEFVKESLNYVTIIGGETCGCL
 DMDQ - - - - - QLARETSVDP - - - DMRKGQLQELKAKGKLVDCKVS
 LTYGILLP - - - - PFIWTLLMPAIALLLRFFANAFTLTPYNNGTEALVWL
 CIGEDPQGIPNN - LMPYVSSQVALGRR - BALNVFGNDYDTEDGTGVRDYI
 VLPPVTL - - DTPMNRKSMPPEADFS - - - SWTPPLEFLVETFDWITGKN

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Fig. 4d-top left

CGI-93	L - L ₂₈₀ W G R R K M - - - - -	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰	³⁵⁰	³⁶⁰	³⁷⁰	³⁸⁰	³⁹⁰
DKFZ-ORF	L - A A V G K K K D V I I L A D L L P S L A V Y L R T L A P G L - - F F S L M A S R A R K E R K S K N S	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰	³⁵⁰	³⁶⁰	³⁷⁰	³⁸⁰	³⁹⁰
CR-1	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
CR-3	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
SRL	S - F I L C I S E D A S Y I T - - G E T V V V G G G T P S R L - - - - -	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
Hep-27	S - F I L C I S P D A S Y V N - - G E N I A V A G - Y S T R L - - - - -	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
SDH-RDH	E - Q K C T Q D L S L V T N C M E H A L I A C H P R T R Y S A G - - W D A K L L Y L P M S Y M P T F L V	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
RODH4	E - Q K C T Q D L S L V T N C M E H A L I A C H P R T R Y S A G - - W D A K L L Y L P M S Y M P T F L V	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
RDH	L - L N C I S T T N L N L V T D C M E H A L T S V H P R T R Y S A G - - W D A K F F I P L S Y L P T S L A	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
9cls-RDH	M N L I C D P D L T K V S R C L E H A L T A R H P R T R Y S P G - - W D A K L L W L P A S Y L P A S L V	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
3beta-HSD-	P K K A P ₂₅₀ I R G Q F Y Y I S D D T P H Q S Y D - - N L N Y T L S K E F G L R L D S R W S F P L S L M Y	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
3beta-HSD-	P K K A P ₂₅₀ V R G Q F Y Y I S D D T P H Q S Y D - - N L N Y I L S K E F G L R L D S R W S L P L T L M Y	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
RDH_ORF	K - S Y V N M D L S P V V E C M D H A L T S L F P K T H Y A A G - - K D A K I F W I P L S H M P A A L Q	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
CGI-86	L - I S M A N D L K E V V W I S B Q P F L L V T Y L W Q Y M P T W - - A W W I T N K M G K K R I E N F K S	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
BDH	C - S S G ₂₅₀ T D T S P V I D A V T H A L T A T T P Y T R Y H P M D - Y Y W W L R M Q I M T H L P G A I S	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
17beta-HSD	N - S ₂₅₀ A ₂₆₀ S K D F S P V L R D I Q H A I I L A K S P F A Y Y T P G - - K G A Y I L W I C L A H Y L P I G I Y	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
11beta-HSD	L - R ₂₅₀ A ₂₆₀ M S D L T P V V D A I T D A L L A A R P R R Y Y P G - - Q G L G I L M Y F I H Y Y L P E G L R	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
CR-AG	L - F ₂₅₀ I L S D R S G M T T G S T L P V B G G F W A C - - - - -	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
11cis-RDH	A - F ₂₅₀ A ₂₆₀ S D E A A Y I T G E T L H V N G G M Y M V - - - - -	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰
17beta-HSD	A - F ₂₅₀ A ₂₆₀ S D S G Y I T G T S V E V T G G L I M - - - - -	²⁴⁰	²⁵⁰	²⁶⁰	²⁷⁰	²⁸⁰	²⁹⁰	³⁰⁰	³¹⁰	³²⁰	³³⁰	³⁴⁰

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.Fig. 4d-top middle

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Fig. 4d-top right

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Fig. 4d-bottom left

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Fig. 4d-bottom middle

P Q S I Q - - - - -
 E T F K E K A K L - - - - -
 K T K G S - - - - -
 R C M M Q R E K S E N A D K T A - - - - -
 A G A E A G G G A G P G A E D E A G R S A V G D P E L G D P P A A P Q - - - - -
 R Y P K W I I A L Y T S K F - - - - -
 V T I Q K T D N Q A R L S G S C L - - - - -
 A S G K K I P Y K V V A R R E G D V A A C Y A N P S L A Q E U E L G W T A A L G L D R - - - - -
 M C E D L W R W Q K Q N P S G F
 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

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Fig. 4d-bottom right